

QY 1 DGGKFFKPSFSS 15
||| ||||| ||
DB 124 DGGKFFKPSFSS 119

RESULT 3

T19629
Experimental protein C32A3.2 *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15 Jul 1999 #Sequence_revision 16 Jul 1999 #next_change 21 Jul 1999
C:Accession: T19629
R:Thomas, K.
Submitted to the EMBL Data Library, February 1995
A:Reference number: T19629
A:Accession: T19629
A:Status: preliminary
A:Superfamily: translated from GP/EMBL/DBP
A:Molecule type: DNA
A:Residues: 1-346 <WIL>
A:Cross-references: EMBL:U42341, FID:CAAG34.1, EMBL:U42341, EMBL:U42341, EMBL:U42341
A:Experimental source: clone C32A3
C:Genetics:
A:Gene: C32A3.2
A:Map position: 3
A:Insertions: 47/3, 75/3, 117/3, 156/3, 156/3

Query Match 50.0% Score 50; DB 2; Length 346;
Best local similarity 100%; Pred No. 12;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DGGKFFKPSFSS 15
||| ||||| ||
DB 4 DGGKFFKPSFSS 15

RESULT 4

S3219
Histone H1 C African clawed frog
C:Species: *Xenopus laevis* (African clawed frog)
C:Date: 06 Jan 1995 #Sequence_revision 06 Jan 1995 #next_change 21 Jul 1999
C:Accession: S3219
R:Schluthuis, J.G.; Hagenaar, M.; Destre, O.H.J.
Submitted to the EMBL Data Library, March 1993
A:Description: preliminary alignments between histone gene clusters in the genome of *Xenopus laevis*
A:Reference number: S32621
A:Accession: S3219
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-221 <SCH>
A:Cross-references: EMBL:X70224, FID:J-94139, FID:CAAG34.3.1, FID:J-94139
C:Superfamily: histone H1

Query Match 50.0% Score 49; DB 2; Length 211;
Best local similarity 100%; Pred No. 16;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 PPKVFFKPSFSS 16
||| ||||| ||
DB 16 PPKVFFKPSFSS 16

RESULT 5

B88481
Protein C16A3.5 (imported) - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 11 May 1999 #Sequence_revision 11 May 1999 #next_change 14 May 1999
C:Accession: B88481
R:Anonymous, The C. elegans Sequencing Consortium.
Science 287, 2132-2139, 1999
A:Title: Genome sequence of the nematode *C. elegans*, a platform for investigating biological processes
A:Reference number: Anonymous, WormBase, 1999
A:Description: preliminary alignments between histone gene clusters in the genome of *Xenopus laevis*
A:Reference number: S32621

A:Accession: B88481
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-323 <STO>
A:Cross-references: GB:chi_III, FID:AA547536.1, FID:41103626, GSF:GB:GN00021, GSF:GB:GN00021
C:Genetics:
A:Gene: C16A3.5
A:Map position: 3
A:Superfamily: VAPC protein

Query Match 50.0% Score 49; DB 2; Length 323;
Best local similarity 64.3%; Pred No. 12;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 PPKVFFKPSFSS 16
||| ||||| ||
DB 277 PPKVFFKPSFSS 290

RESULT 6

A54693
CACC box-binding protein beta - human
C:Species: *Homo sapiens* (man)
C:Date: 23 Mar 1995 #Sequence_revision 23 Mar 1995 #next_change 21 Jul 1999
C:Accession: A54693
R:Wang, Y.; Kobori, A.; Hood, L.
Submitted to the EMBL Data Library, 13 May 1993
A:Reference number: A54693; EMBL:U42341; FID:U42341
A:Accession: A54693
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-454 <WAN>
A:Cross-references: GB:U04282
C:Keywords: DNA binding; T-cell; transcription regulation; zinc finger

Query Match 50.0% Score 49; DB 2; Length 454;
Best local similarity 64.3%; Pred No. 16;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 PPKVFFKPSFSS 16
||| ||||| ||
DB 313 PPKVFFKPSFSS 326

RESULT 7

T41622
T41622 APC transporter fission yeast (schizosaccharomyces pombe)
C:Species: *Schizosaccharomyces pombe*
C:Date: 03 Apr 1999 #Sequence_revision 03 Apr 1999 #next_change 21 Jul 1999
C:Accession: T41622
R:Aert, P.; Volckart, G.; McDonnell, P.C.; Pandreem, M.A.; Bartell, R.G.
Submitted to the EMBL Data Library, October 1999
A:Reference number: T41735
A:Accession: T41622
A:Status: preliminary; translated from GB/EMBL/DBP
A:Molecule type: DNA
A:Residues: 1-922 <AER>
A:Cross-references: EMBL:U42341, FID:CAAG34.3.1, FID:U42341, FID:U42341, FID:U42341
C:Genetics:
A:Gene: SPBR:SPC0825.01
A:Map position: 3

Query Match 57.8% Score 48; DB 2; Length 822;
Best local similarity 62.9%; Pred No. 37;
Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 4 PPKVFFKPSFSS 16
||| ||||| ||
DB 100 PPKVFFKPSFSS 102

cy 3 PKKKKKSPSKSSS 16
| : | : | | | |
db 45 PGNFKTGPCKSSS 58

3
4
5
6
7
8
9

accession: 10
 T11744
 dehydrin kidney bean
 GenBank accession: F54316 (P. H. Y. Tang)
 CSpecies: Phaseolus vulgaris
 CDate: In duplicate sequence revision 16 Jul 1993
 CAccession: T11744
 CAuthor: F. Chai, T. Y. Burkard, G.
 Submitted to the EMBL Data Library, April 1996
 AReference number: 21330
 AAccession: T11744
 AStatus: preliminary; translated from GR/EMBL/DBJ
 AMolecule type: mRNA
 APosition: 1-622 CDS
 ACross references: EMBL:U54769, NID:U54769, F10:U54761
 AExperimental source: cultivar saxa
 ANotes: regulated by dehydration stress, elevated in the APB, heavy metal stress, and wounding
 Keywords: stress-induced protein

Query Match:	54.2%	Score 45, BP 2,	Long+K 202;
Best Local Similarity:	59.2%	Page No. 29;	
Matches:	5;	Mismatches	4; Inlets

Cy 1 DGPFFFFFSSSK 13
| | | | |
Db 87 DGFFKKKKKKK 99

RESULT : 4

[illegible]

Query Match 54.2%; Score 45; DB 2; Length 203;
Best Local Similarity 61.5%; Pred. No. 29;
Matches 8; Conservative 2; Mismatches 3; Indels

Q7	3	PRKAFKSSPKSS	15
			:
D6	195	PRKAFKSPKFA	197

RECEIVED 15

T17250
 hypothetical protein YP756c1022.1 - human
 C1:Species: Homo sapiens (man)
 C1:Date: 15-Oct-1999 #sequence_revision 1-000-1999
 C1:Accession: T17250
 R1:Kocher, K.J.; Beyer, A.; Mewes, H.W.; Gasteiger, J.; Wilmann, S.
 submitted to the Protein Sequence Database, September 1999
 A:Reference number: Z18772
 A:Accession: T17250
 A>Status: preliminary

A. Molecule type: mRNA
A. Peptides: 1-482 rPE
A. Cross references: EMBL:AL117465
A. Experimental source: adult uterus; clone D5F2p58c1032
C. Genetics: 1
A. Refs: D5F2p58c1032; 1

Query Match: 54.28; Score: 45; DP: 2; length: 482;
Posterior similarity: 0.00; Evid: 10; 61;
Matches: 9; Conservative: 1; Mismatches: 5; Indels:

```
00      1 nGpKkKKKKcPSS 15
01      22 hPaPyKkKdVdd 106
```

Search completed: March 3, 2003, 06:25:25

us-09-214-913-37.rsp

Mon Mar 3 10:55:21 2003

GN MLP OR MRP.
OS Oryctolagus cuniculus (Rabbit).
EC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
CX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
PC TISSUE=Macrophage;
RA MEDLINE=2038550; PubMed=1516135;
RA Li J., Adenem A.;
RT "MacMARCKS, a novel member of the MARCKS family of protein kinase C
RT substrates.";
RL Cell 70:791-801 (1992).
CC -!- FUNCTION: MAY BE INVOLVED IN COUPLING THE PROTEIN KINASE C AND
CC -!- CALMODULIN SIGNAL TRANSDUCTION SYSTEMS.
CC -!- PTM: PHOSPHORYLATED.
CC -!- SIMILARITY: BELONGS TO THE MARCKS FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC -----
CC EMBL; S43921; AAB23156.1; --
CC DR PIR; A43341; A43341; MARCKS
CC DR InterPro; IPR002101; MARCKS
CC DR Pfam; PF02063; MARCKS; 1
CC DR PRINTS; PR00963; MARCKS.
CC DR PROSITE; PS00826; MARCKS_1; 1.
CC DR PROSITE; PS00827; MARCKS_2; 1
CC KW Phosphorylation; Myristate; Calmodulin-binding.
FT INIT_MET 0 0
FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
FT DOMAIN 96 99 CALMODULIN BINDING (ESD). (BY SIMILARITY).
FT MOD_RES 92 92 PHOSPHORYLATION (BY PFC) (BY SIMILARITY).
FT MOD_RES 100 100 PHOSPHORYLATION (BY PFC) (BY SIMILARITY).
FT MOD_RES 103 103 PHOSPHORYLATION (BY PFC) (BY SIMILARITY).
SQ SEQUENCE 198 AA; 19635 MW; 6032A7E1E6D9CD4A CYS764;
Query Match 52.4%; Score 43.5; DB 1; Length 198;
Best Local Similarity 64.7%; Pred. No. 13; Mismatches 3; Gaps 1;
Matches 11; Conservative 0;
Cy 3 FXXXXX KPSKSSG 16
Db 95 PXXXXXSKPPPLSG 101

Search completed: March 3, 2003, 06:36:17
Job time : 24.6585 secs

17	47	56.6	422	16	C67823	C67823 arabidops
18	46.5	56.0	320	5	Q9NSP5	Q9NSP5 caenorhabd
19	46	55.4	312	4	Q14568	Q14568 homo sapien
20	46	55.4	315	4	Q8H4J8	Q8H4J8 homo sapien
21	46	55.4	318	3	Q9HEU6	Q9HEU6 caenorhabd
22	46	55.4	421	5	Q9BL72	Q9BL72 caenorhabd
23	46	55.4	463	5	Q9VB74	Q9VB74 arabidops
24	46	55.4	464	4	Q961C9	Q961C9 homo sapien
25	46	55.4	488	4	Q96NM4	Q96NM4 homo sapien
26	46	55.4	526	4	Q94900	Q94900 homo sapien
27	46	55.4	526	4	Q96AV5	Q96AV5 homo sapien
28	46	55.4	526	11	Q9P4H0	Q9P4H0 mus musculu
29	46	55.4	537	5	Q9VTJ6	Q9VTJ6 arabidops
30	46	55.4	573	13	Q9PST7	Q9PST7 xenopus lae
31	46	55.4	573	13	P70045	P70045 xenopus lae
32	46	55.4	699	5	Q9VSD4	Q9VSD4 arabidops
33	46	55.4	702	5	Q9V109	Q9V109 arabidops
34	46	55.4	897	5	Q71336	Q71336 caenorhabd
35	46	55.4	8282	5	Q9RKG4	Q9RKG4 arabidops
36	45.5	54.8	930	10	Q9LU74	Q9LU74 arabidops
37	45	54.2	67	16	Q9K88C	Q9K88C arabidops
38	45	54.2	101	15	Q9UMW6	Q9UMW6 homo sapien
39	45	54.2	160	11	Q9D025	Q9D025 mus musculu
40	45	54.2	202	10	Q41111	Q41111 pascuobu
41	45	54.2	211	13	Q9CGK5	Q9CGK5 arabidops
42	45	54.2	277	11	Q9C8A2	Q9C8A2 mus musculu
43	45	54.2	286	11	Q9C8A5	Q9C8A5 mus musculu
44	45	54.2	409	13	Q9CGN9	Q9CGN9 arabidops
45	45	54.2	450	11	Q9DA19	Q9DA19 mus musculu

Version 5.1.1
Copyright 1999
File: Search time 14.11 seconds
without alignment
94.921 Million bits
94.921 Million bits

ALIGNMENTS

RESULT 1

Q94AY9

ID Q94AY9 PRELIMINARY; PRT: 162 AA.

AC Q94AY9

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE AT5G41020/MEE6.9 (Fragment).

OS Arabidopsis thaliana (Mouse-ear cress).

CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta

CC Spermatophyta; Magnoliopsida; Eudicotyledones; Core eudicotyledones; Eu

CC eudicotyledones; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Kuesema E., Chen H., Cheek P., Kim C.J., Meyers M.C., Shinn P.,

RA Bann J., Rowser L., Carninci P., Dale J.M., Gibson H.A.,

RA Goldsmith A.D., Hayashizaki Y., Ishida J., Liang P.X., Maher T.,

RA Kamiya A., Karim Neumann G., Kawai J., Lam P., Lee C.M., Liu X.,

RA Liu S.X., Miranda M., Narusaka M., Nguyen M., Ohtera M., Ohtera T.,

RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Shimazaki A.,

RA Tang C.C., Terakawa M., Yamada K., Yu G., Yu S., Shimazaki A.,

RA Davis P.W., Teichgraber A., Ecker J.R.,

RA "Arabidopsis CDNA clones."

RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

PL EMBL: AY045603; AAC13961.1;

DE EMBL: AY045603; AAC13961.1;

FI NON TER 162

CC SEQUENCE 162 AA, 184.4 MW, 162.5504 kDa, pI 4.84

Query Match 61.4%; Score 51; DB 10; Length 162

Best Local Similarity 62.5%; Fred. No. 12;

Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0

QV 1 DDPKVVVVVSPKSSG 14

DB 133 DGVVKKKKKKSSG 148

RESULT 2

QY 3 PRKPKKSPKSSG 16
|||||
Db 19 PRKPKKSPKSSG 31
Mismatches 4; Indels 0; Gaps 0;

RESULT 7
Q91XQ7 PRELIMINARY; PRT; 287 AA.
AC Q91XQ7; (REBELrel. 19, Created:
DT 01-DEC-2001 (REBELrel. 19, Last sequence update
DT 01-DEC-2001 (REBELrel. 19, Last sequence update
DT 01-JUN-2002 (REBELrel. 21, Last annotation update)
DE G-rich box-binding protein Berf-1 variant, Fragment
GN ZFP148.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD-1; TISSUE=LMB;
RX MEDLINE=21322871; PubMed=11322790;
RA Leo S., Antona V., Cammarata G., Cavaleri F., Passantino S.,
RA Rabino P., Giallongo A.;
RT "Conserved structure and promoter sequence similarity in the mouse and
RT human genes encoding the zinc finger factor BERF-1/BERF1/BERF1L2/BERF1L3;
RL Biochem Biophys Res Commun. 283:229-238/2001.
DR EMBL; AF316550; AAK63005.1; -.
DP MCD; MG1:132224; Zfp148
FT NON-TER 1
FT SEQUENCE 287 AA; 2184 MW; 4E0410E09F38B4 CP5647;

Query Match 59.0%; Score 49; IR 11; Length 287;
Best Local Similarity 64.1%; Pred. No. 4.3;
Matches 9, Conservative 3, Mismatches 2, Indels 0, Gaps 0;

QY 3 PRKPKKSPKSSG 16
|||||
Db 49 PRKPKKSPKSSG 61
Mismatches 0; Indels 0; Gaps 0;

RESULT 8
Q18035 PRELIMINARY; PRT; 311 AA.
AC Q18035;
DT 01-NOV-1994 (REBELrel. 31, Created:
DT 01-NOV-1994 (REBELrel. 31, Last sequence update)
DT 01-DEC-2001 (REBELrel. 19, Last annotation update)
DE Hypothetical 17.9 kDa protein.
GN Cl6A3.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Phadodrida; Flatulidra;
OC Phaditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID:6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium;
RL Science 283:2281-2281/1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Favallo A.;
RT "The sequence of C. elegans cosmid Cl6A3.6";
RN Submitted (DEC-1995) to the EMBL/GenBank/CCDB databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;

QY 3 PRKPKKSPKSSG 16
|||||
Db 19 PRKPKKSPKSSG 31
Mismatches 4; Indels 0; Gaps 0;

RESULT 7
Q91XQ7 PRELIMINARY; PRT; 287 AA.
AC Q91XQ7; (REBELrel. 19, Created:
DT 01-DEC-2001 (REBELrel. 19, Last sequence update
DT 01-DEC-2001 (REBELrel. 19, Last sequence update
DT 01-JUN-2002 (REBELrel. 21, Last annotation update)
DE G-rich box-binding protein Berf-1 variant, Fragment
GN ZFP148.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD-1; TISSUE=LMB;
RX MEDLINE=21322871; PubMed=11322790;
RA Leo S., Antona V., Cammarata G., Cavaleri F., Passantino S.,
RA Rabino P., Giallongo A.;
RT "Conserved structure and promoter sequence similarity in the mouse and
RT human genes encoding the zinc finger factor BERF-1/BERF1/BERF1L2/BERF1L3;
RL Biochem Biophys Res Commun. 283:229-238/2001.
DR EMBL; AF316550; AAK63005.1; -.
DP MCD; MG1:132224; Zfp148
FT NON-TER 1
FT SEQUENCE 287 AA; 2184 MW; 4E0410E09F38B4 CP5647;

Query Match 59.0%; Score 49; IR 11; Length 287;
Best Local Similarity 64.1%; Pred. No. 4.3;
Matches 9, Conservative 3, Mismatches 2, Indels 0, Gaps 0;

QY 3 PRKPKKSPKSSG 16
|||||
Db 49 PRKPKKSPKSSG 61
Mismatches 0; Indels 0; Gaps 0;

RESULT 8
Q18035 PRELIMINARY; PRT; 311 AA.
AC Q18035;
DT 01-NOV-1994 (REBELrel. 31, Created:
DT 01-NOV-1994 (REBELrel. 31, Last sequence update)
DT 01-DEC-2001 (REBELrel. 19, Last annotation update)
DE Hypothetical 17.9 kDa protein.
GN Cl6A3.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Phaditidae; Flatulidra;
OC Phaditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID:6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium;
RL Science 283:2281-2281/1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Favallo A.;
RT "The sequence of C. elegans cosmid Cl6A3.6";
RN Submitted (DEC-1995) to the EMBL/GenBank/CCDB databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;

11	83	100.0	215	19	AAW75990	Human polyepitide
12	83	100.0	215	19	AAW75992	Human polyepitide
13	83	100.0	215	19	AAW75994	Human polyepitide
14	77	92.8	16	21	AAW45881	Human polyepitide
15	77	92.8	16	21	AAW58858	Human polyepitide
16	77	92.8	16	21	AAW58859	Human polyepitide
17	77	92.8	16	21	AAW58860	Human polyepitide
18	77	92.8	16	21	AAW58861	Human polyepitide
19	52	62.7	55	23	ABP33749	Human polyepitide
20	52	62.7	55	23	ABP33750	Human polyepitide
21	51	61.4	115	22	AAO55774	Human polyepitide
22	50	60.2	115	22	AAO55775	Human polyepitide
23	50	60.2	126	22	AAO55776	Human polyepitide
24	50	60.2	2029	22	AAO55777	Human polyepitide
25	49	59.0	141	22	AAU27443	Human polyepitide
26	49	59.0	141	22	AAU27444	Human polyepitide
27	49	59.0	154	22	AAU27445	Human polyepitide
28	49	59.0	511	22	ABG23339	Human polyepitide
29	49	59.0	794	23	ABG23340	Human polyepitide
30	48	57.8	53	22	AAO55000	Human polyepitide
31	48	57.8	147	22	AAO55001	Human polyepitide
32	48	57.8	177	21	AAO55002	Human polyepitide
33	48	57.8	192	21	AAO55003	Human polyepitide
34	48	57.8	201	21	AAO55004	Human polyepitide
35	47	56.6	33	22	AAO55005	Human polyepitide
36	47	56.6	80	22	AAO55006	Human polyepitide
37	47	56.6	80	22	AAO55007	Human polyepitide
38	46	55.4	242	13	AAO55008	Human polyepitide
39	46	55.4	17	18	AAW38764	Human polyepitide
40	46	55.4	21	22	AAW38765	Human polyepitide
41	46	55.4	25	22	AAW38766	Human polyepitide
42	46	55.4	89	22	AAW38767	Human polyepitide
43	46	55.4	93	22	AAW38768	Human polyepitide
44	46	55.4	107	22	AAW38769	Human polyepitide
45	46	55.4	116	22	AAW38770	Human polyepitide

ALIGNMENTS

RESULT 1
AAW45878
ID AAW45878 standard; peptide; 16 AA.
XX
AC AAW45878;
XX
XX 30-JUN-1999 (first entry)
XX Peptide membrane binding element.
XX
XX Membrane binding element, thrombotic disease; inflammatory
XX Complement related disease; soluble peptide.
XX Synthetic.
XX
XX WC9802454 A2.
XX
XX 22-JAN-1998.
XX
XX 08-JUL-1997; 97WO EP01715.
XX
XX 15-JUN-1996; 96SB-0014871.
XX
XX (ADPR-) ADPROTECH PLC.
XX
XX Dodd I, Mossakowska DEU, Smith FAG;
XX
XX WFI, 1105/4/10.
XX
XX Derivatives of soluble polyepitides bonded to low affinity
XX membrane binding groups - useful for treating complement-related and
XX thrombotic diseases, providing improved inhibition at cellular
XX membranes

results predicted by this tool have a
to the score of the tool. The printed
the total score distribution.

SYNOPSIS

AAW45878 Peptide membrane b
AAW45879 Membrane binding e
AAW45880 Antithrombotic mem
AAW45881 Peptide membrane b
AAW45882 Peptide binding e
AAW45883 Amino acid sequenc
AAW45884 Amino acid sequenc
AAW45885 Amino acid sequenc
AAW45886 Complement recepto
AAW45887 Complement recepto

sp. particularly associated with resistant
useful as wound treatment agents to
treatly proteins, especially fibrinogen,
or prophylactic use in dental treatment as
cation with, antibiotic prophylaxis. (1)
in membranes which have a higher
pH than the eukaryotic organisms, also
membrane associated proteins, also
antimicrobial activity upon derivatization
that the antibiotic resistant bacterial
represent peptides given in the
invention

Seq. A1; DP 23; Domain 1;
Prod. No. 8,10-34;
Mismatches 0; Gaps 0;

AA;

DP;

sp. disease; s (10-11-12);
central membrane protein; inflammation.

DP 23;

sp. s. bonded; low affinity
cell for treating compound related and
improved localization of cellular

AA;

represents a specifically claimed membrane
relates to a soluble derivative (A) of a
a comprises at least a heterologous
of low membrane affinity, covalently
and, independently and with thermodynamic
cellular or artificial membranes ex-
are used to treat disorders treatable with
removal or any other complement-related
enzyme, graft rejection, myocardial
inflammation and many others, including
leukemia and thrombolytic disease, but also to
cells, to treat ischemic or infarcted and as
multiple sclerosis. A also administered

CC orally, topically, by injection or inhalation at 0.01-10 mg/kg/day.

XX Sequence 17 AA;

Query Match 100.0%; Score A1; DP 19; Length 17;
Best Local Similarity 100.0%; Prod. No. 8,10-34;
Matches 16; Conservative 0; Mismatches 0; Gaps 0;

CY 1 DGPYKPKKPKKSSG 16
DB 1 DGPYKPKKPKKSSG 16

RESULT 5

AAV5862

ID AAY58862 standard; Peptide; 17 AA.

XX AC AAY58862;

XX DT 08-MAY-2000 (first entry)

XX DE Membrane binding element used in anti-angiogenic polypeptide.

XX KW Anti-angiogenic, angiogenesis inhibitor; membrane binding element;

XX KW cancer; tumour; therapy.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Modified-site /note= "nyristoylated"

XX PN WC200004052-A2.

XX PO 27-JAN-2000.

XX PF 16-JUL-1999; 99WO 0802292.

XX PR 16-JUL-1998; 98GB-0015505.

XX PA (ADPR-) ADPROTECH PLC.

XX PI Smith RAG, Bright JR, Steward M, Cox VF;

XX DE WPI; 2000-182406/16.

XX New soluble derivative of anti-angiogenic polypeptide useful for
treatment of primary or secondary tumours, and also potentially attached
membrane-binding elements for targeting
PS Disclosure, Page 13; 36pp; English.
XX The present sequence is an example of a lysine-rich peptide
membrane binding element (MBE) that can be utilised in novel
soluble derivatives (1) of anti-angiogenic polypeptides of the
invention (2) comprising 2 or more heterologous MBEs with low
membrane affinity that are covalently attached to a soluble
anti-angiogenic polypeptide such as a non-catalytic region of human
plasminogen, fragments of related proteins containing kinase
domains, fragments of collagen or prolactin, neutralising
antibodies against receptors for angiogenic mediators, and
an array of fragments involved in cell adhesion. The MBEs
interact independently with thermodynamic additivity, with
conformations of the vascular endothelium. provide targeted
delivery of the anti-angiogenic polypeptide to cell membranes and
sites of active angiogenesis, particularly the vascular endothelium,
and therefore increase the local concentration and reduce the risk
of adverse effects on normal processes elsewhere in the vasculature.
They are used in a claimed method of treatment of primary or
secondary tumour.

XX Sequence 17 AA;

CC shock), autoimmune diseases (e.g. rheumatoid arthritis, systemic lupus
 erythematosus, hemolytic anemia, glomerulonephritis and vasculitis),
 CC graft-versus-host disease, idiopathic myelofibrosis, aplastic
 anemia, and various disorders involving the immune system. The present sequence represents the
 CC amino acid sequence of APT2065.
 XX
 SQ Sequence 88 AA;
 Query Match 100.0%; Score 83; DB 23; Length 88;
 Best Local Similarity 100.0%; Field No. 4.4e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QV 1 DGPYKFKYKSPKSSG 16
 |||||
 DB 73 DGPYKFKYKSPKSSG 88
 |||||
 RESULT 7
 ABB07538
 ID ABB07538 standard; peptide; 99 AA.
 XX
 AC ABB07538;
 XX
 DT 23 APR 2002 (first entry)
 DE Amino acid sequence of APT2062.
 XX
 KW CDS9; lipid raft derivative; CAS; neuroprotective; neurotropic; human;
 KW cerebroprotective; antiparkinsonian; antiallergic; antitumor; cardiac;
 KW antidiabetic; antidiabetic; dermatological; hypertensive; vasotropic;
 KW antitumor; antitumor; antitumor; antitumor; antitumor;
 KW immunosuppressive; antitumor; neurotropic; antitumor;
 KW antitumor; antitumor; antitumor; antitumor; antitumor;
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Disulfide bond 92..93 /note= "disulfide bridge"
 XX
 PN WC000204638-A1.
 XX
 PD 17 JAN 2002.
 XX
 PE 06-JUL-2001; 2001W0 GB003034.
 XX
 PF 07-JUL-2000; 2000GB-0016811.
 XX
 PA (ADPR-) ADPR0TECH LTD.
 XX
 PI Rowling RUE, Smith GP, Ridley SH;
 XX
 WP; 2002-164646/21.
 XX
 CC The present invention is a soluble derivative (D) of a soluble
 peptide (P). It has two cysteine residues which form an intramolecular disulfide bond. The peptide has a low membrane affinity covalently associated with the polypeptide.
 CC the elements being capable of interacting with components of cellular or
 CC artificial membranes exposed to extracellular fluids and target lipid
 CC raft components of membrane. It is useful for treating disorders
 CC associated with treatment by a soluble peptide fragment (P), CAS or other
 CC (e.g., CDS9), and for the preparation of a reagent for treatment
 CC of disorders involving complement activity and various inflammatory and
 CC immune disorders. It is useful for treating neurological disorders (e.g.,
 CC multiple sclerosis, stroke, Parkinson's, Alzheimer's disease, traumatic
 CC brain injury and allergic encephalitis), disorders of macrophage or
 CC undesirable complement activation (e.g., xenograft rejection, neuronal
 CC graft rejection), inflammatory disorders (including allergic rhinitis,
 CC asthma, bronchitis, eczema, psoriasis, asthma, eczema, acute
 CC inflammation), post-ischemic reperfusion conditions (e.g., myocardial
 CC infarction, hypotension, cerebral ischemia, stroke, atherosclerosis),
 CC infection, blood vessel injury (e.g., atherosclerosis, stroke,

CC Query Match 100.0%; Score 83; DB 23; Length 17;
 Best Local Similarity 100.0%; Field No. 4.4e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QV 1 DGPYKFKYKSPKSSG 16
 |||||
 DB 73 DGPYKFKYKSPKSSG 88
 |||||
 RESULT 6
 ABB07540
 ID ABB07540 standard; peptide; 98 AA.
 XX
 AC ABB07540;
 XX
 DT 23 APR 2002 (first entry)
 DE Amino acid sequence of APT2065.
 XX
 KW CDS9; lipid raft derivative; CAS; neuroprotective; neurotropic; human;
 KW cerebroprotective; antiparkinsonian; antiallergic; antitumor; cardiac;
 KW antidiabetic; antidiabetic; dermatological; hypertensive; vasotropic;
 KW antitumor; antitumor; antitumor; antitumor; antitumor;
 KW immunosuppressive; antitumor; neurotropic; antitumor;
 KW antitumor; antitumor; antitumor; antitumor; antitumor;
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Disulfide bond 91..92 /note= "disulfide bridge"
 XX
 PN WC000204638-A1.
 XX
 PD 17 JAN 2002.
 XX
 PE 06-JUL-2001; 2001W0 GB003034.
 XX
 PF 07-JUL-2000; 2000GB-0016811.
 XX
 PA (ADPR-) ADPR0TECH LTD.
 XX
 PI Rowling RUE, Smith GP, Ridley SH;
 XX
 WP; 2002-164646/21.
 XX
 CC The present invention is a soluble derivative (D) of a soluble
 peptide (P). It has two cysteine residues which form an intramolecular disulfide bond. The peptide has a low membrane affinity covalently associated with the polypeptide.
 CC the elements being capable of interacting with components of cellular or
 CC artificial membranes exposed to extracellular fluids and target lipid
 CC raft components of membrane. It is useful for treating disorders
 CC associated with treatment by a soluble peptide fragment (P), CAS or other
 CC (e.g., CDS9), and for the preparation of a reagent for treatment
 CC of disorders involving complement activity and various inflammatory and
 CC immune disorders. It is useful for treating neurological disorders (e.g.,
 CC multiple sclerosis, stroke, Parkinson's, Alzheimer's disease, traumatic
 CC brain injury and allergic encephalitis), disorders of macrophage or
 CC undesirable complement activation (e.g., xenograft rejection, neuronal
 CC graft rejection), inflammatory disorders (including allergic rhinitis,
 CC asthma, bronchitis, eczema, psoriasis, asthma, eczema, acute
 CC inflammation), post-ischemic reperfusion conditions (e.g., myocardial
 CC infarction, hypotension, cerebral ischemia, stroke, atherosclerosis),
 CC infection, blood vessel injury (e.g., atherosclerosis, stroke,

FT Peptide /label= CM16/cys
FT 199..215
FT /label= MSWP-1
FT Disulfide-bond 199..199
FT Modified-site 199
FT /note= "(S-2-thiopyridyl) cysteine"
FT Modified-site 215
FT /note= "N-(myristoyl) glycine"
XX PN WC9839433-A1.
XX XX
XX PD 11-SEP-1998.
XX XX
XX 05-MAR-1998; 98WC-GB0727.
XX XX
XX 05-MAR-1997; 97GB-0004519.
XX XX
XX (ADPR-) ADPROTECH PLC.
XX Cux VF, Mossakowska DE1, Smith RAG;
XX WFI, 1992-1993/43.
XX XX
XX Soluble polypeptide comprising short consensus repeats from the A
XX used to treat disorders and diseases associated with inflammation or
XX inappropriate complement activation
XX PS Claim 17; Page 56; 67pp; English.
XX XX
XX This is the amino acid sequence of CM16. Cys-S-MSWP-1
XX comprising novel soluble complement receptor type 1 (CR1) like
XX polypeptide CM16 joined to a myristoylated lipidic switch, peptide
XX reagent 1 (MSWP-1). It was produced by cloning CM16/cys (see
XX AA075989) to a synthetic MSWP-1 peptide (see AA075989). CM16 comprises
XX the short consensus repeats (Scp) from CR1 in which 21 amino acid
XX residues are substituted by those corresponding to the CR1-like
XX protein, soluble CR1, derived from human plasma. The amino acid
XX sequence is 199..215. CM16 acts as complement inhibitors with
XX functional complement inhibitory, including anti-haemolytic,
XX activity. These can be used to treat a disease or disorder
XX associated with inflammation or inappropriate complement activation,
XX such as neurological disorders (e.g. multiple sclerosis, Parkinson's
XX disease), disorders of inappropriate or undesirable complement
XX activation (e.g. xenograft rejection), inflammatory disorders (e.g.
XX Crohn's disease, asthma, and acute pancreatitis), post-ischaemic
XX reperfusion conditions, infection or sepsis, immune complex
XX disorders and autoimmune diseases (e.g. rheumatoid arthritis,
XX proliferative nephritis and myasthenia gravis), and reproductive
XX disorders.
XX SQ Sequence 215 AA;
Query Match 100.0%; Score 91, 92 19, Length 215;
Best local similarity 100.0%; Pident. No. 0.0001;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DGPRTYKPKSPKSSG 16
DB 200 DGPRTYKPKSPKSSG 215
RESULT 13
APB07542
ID ABB07542 standard; peptide; 27; AA.
XX AC ABB07542;
XX XX
XX 23-APR-2002 (first entry)
XX DE Amino acid sequence of APT2334.
XX KW CDS9; lipid raft derivative; DAF; neuroprotective; neurotrophic factor;
XX cerebroprotective; antiparkinsonian; anti-allergic; antitubercular;

FT Peptide /label= CM16/cys
FT 199..215
FT /label= MSWP-1
FT Disulfide-bond 199..199
FT Modified-site 199
FT /note= "(S-2-thiopyridyl) cysteine"
FT Modified-site 215
FT /note= "N-(myristoyl) glycine"
XX PN WC9839433-A1.
XX XX
XX PD 11-SEP-1998.
XX XX
XX 05-MAR-1998; 98WC-GB0727.
XX XX
XX 05-MAR-1997; 97GB-0004519.
XX XX
XX (ADPR-) ADPROTECH PLC.
XX Cux VF, Mossakowska DE1, Smith RAG;
XX WFI, 1992-1993/43.
XX XX
XX Soluble polypeptide comprising short consensus repeats from the A
XX used to treat disorders and diseases associated with inflammation or
XX inappropriate complement activation
XX PS Claim 17; Page 56; 67pp; English.
XX XX
XX This is the amino acid sequence of CM16. Cys-S-MSWP-1
XX comprising novel soluble complement receptor type 1 (CR1) like
XX polypeptide CM16 joined to a myristoylated lipidic switch, peptide
XX reagent 1 (MSWP-1). It was produced by cloning CM16/cys (see
XX AA075989) to a synthetic MSWP-1 peptide (see AA075989). CM16 comprises
XX the short consensus repeats (Scp) from CR1 in which 21 amino acid
XX residues are substituted by those corresponding to the CR1-like
XX protein, soluble CR1, derived from human plasma. The amino acid
XX sequence is 199..215. CM16 acts as complement inhibitors with
XX functional complement inhibitory, including anti-haemolytic,
XX activity. These can be used to treat a disease or disorder
XX associated with inflammation or inappropriate complement activation,
XX such as neurological disorders (e.g. multiple sclerosis, Parkinson's
XX disease), disorders of inappropriate or undesirable complement
XX activation (e.g. xenograft rejection), inflammatory disorders (e.g.
XX Crohn's disease, asthma, and acute pancreatitis), post-ischaemic
XX reperfusion conditions, infection or sepsis, immune complex
XX disorders and autoimmune diseases (e.g. rheumatoid arthritis,
XX proliferative nephritis and myasthenia gravis), and reproductive
XX disorders.
XX SQ Sequence 215 AA;
Query Match 100.0%; Score 91, 92 19, Length 215;
Best local similarity 100.0%; Pident. No. 0.0001;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DGPRTYKPKSPKSSG 16
DB 200 DGPRTYKPKSPKSSG 215
RESULT 13
APB07542
ID ABB07542 standard; peptide; 27; AA.
XX AC ABB07542;
XX XX
XX 23-APR-2002 (first entry)
XX DE Amino acid sequence of APT2334.
XX KW CDS9; lipid raft derivative; DAF; neuroprotective; neurotrophic factor;
XX cerebroprotective; antiparkinsonian; anti-allergic; antitubercular;

KW antiplatelet; antithrombotic; dermatological; hypertensive; vasorelaxant;
 KW antineoplastic; antiarthritic; antiinflammatory; epidermologicial;
 KW immunosuppressive; antianemic; hepatoprotective; antidiabetic;
 KW antibacterial; antithrombotic; antithrombotic; antithrombotic;
 XX Synthetic;
 OS Homo sapiens.

XX Key Location/Califiers
 FT Disulfide-bond 254-255
 FT Modified-site 271
 FT Note "C-terminal NH myristoyl"

XX W02020204619 A1.

XX 17 JAN 2002.

XX 06-JUL-2001; 2001WO-0503034.

XX 07-JUL-2001; 2000GB-0018011.

XX (ADPR) ADPROTECH LTD.

XX Rowling RUE, Smith GP, Ridley SH;

XX WPI, 2001-10-04-10.

XX Lipid raft targeted derivative of a soluble polypeptide e.g. a soluble
 FT complement regulatory molecule for treating disorders involving
 PT complement activity and various inflammatory, neurological and immune
 PT disorders

XX Claim 5; Page 42; 51pp; English.

XX The invention relates to a soluble derivative (I) of a soluble
 CC polypeptide (II) has two or more heterologous membrane binding elements
 CC with low membrane affinity covalently associated with the polypeptide,
 CC the elements being capable of interacting with components of cellular or
 CC artificial membranes exposed to extracellular fluids and target lipid
 CC and components of membrane. (I) is useful for treating disorders
 CC amenable to treatment by a soluble peptide fragment of 6559, 146 or other
 CC peptides, e.g. 146, and the preparation of a conjugate for treatment
 CC of the disorders involving complement activity and various inflammatory and
 CC immune disorders. (I) is useful for treating neurological disorders, e.g.
 CC multiple sclerosis, stroke, Parkinson's disease, Alzheimer's disease, traumatic
 CC brain injury, inflammatory demyelination, ischemic encephalopathy, traumatic
 CC undesirable complement activation (e.g. xenograft rejection, bacterial
 CC graft rejection), inflammatory disorders (including ulcerative colitis,
 CC Crohn's disease, uveitis, psoriasis, asthma, scleroderma, acute
 CC pancreatitis), post-ischaemic reperfusion conditions (e.g. myocardial
 CC infarction, hypertension, renal ischaemia, restenosis, other cerebrovascular
 CC infarctions), diseases of sepsis (e.g. multiple organ failure, septic
 CC shock), autoimmune diseases (e.g. rheumatoid arthritis, systemic lupus
 CC erythematosus, haemolytic anemia, glomerulonephritis and myasthenia
 CC gravis), reproductive disorders (infertility or complement mediated
 CC infertility), and wound healing. The present sequence represents the
 CC amino acid sequence of A172334.

XX Sequence 271 AA;

Query Match 100.0%; Score 83; DB 23; Length 271;

Best Local Similarity 100.0%; Prod No 0.00014;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDPKPKKPKKSPKSSG 16

DB 256 DDPKPKKPKKSPKSSG 271

RESULT 14

AAW45991

AAW45991 standard; peptide; 16 AA.

XX AAW45991;
 XX 20 MAY 2000 (first entry)
 XX Peptide membrane binding element.
 XX Membrane binding element; thrombotic disease; inflammation;
 XX complement-related disease; soluble peptide.
 XX Synthetic.
 XX W00002454-A2.

XX 22 JAN 1998.

XX 08-JUL-1997; 97WO-EP03715.

XX 15-JUL-1996; 96GR-0014871.

XX (ADPR) ADPROTECH PLC.

XX Dods I, Mossakowska DEI, Smith RAG;

XX WPI, 1998-11-05-24/10.

XX Derivatives of soluble (I) by peptide (I) linked to low affinity
 PT membrane binding groups - useful for treating complement-related and
 PT thrombotic diseases, providing improved localization at cellular
 PT membranes

XX Claim 11, Page 70, 75pp, English.

XX The present peptide sequence represents a specifically claimed membrane-
 CC binding element. The invention relates to a soluble derivative (A) of a
 CC soluble polypeptide (II), which comprises at least 2 heterologous
 CC membrane-binding elements (MBE) of low membrane affinity covalently
 CC associated with (I). MBE interact, independently and with synergistic
 CC activity, with components of cellular and artificial membranes exposed
 CC to extracellular fluids. (A) are used to treat disorders treatable with
 CC (I) itself, specifically inflammation, e.g. the complement-related
 CC disorder (e.g. neurological disease), graft rejection, myocardial
 CC infarction, sepsis, the dermal diseases and many others, including
 CC application to swelling reduction and rheumatoid disease, but also to
 CC treatment of asthma, stroke, weight loss, Crohn's disease or asthma and as
 CC immunomodulators for treating multiple sclerosis. (A) are administered
 CC orally, preferably by ingestion or inhalation at a dose preferably
 CC of 1-100 mg/kg/day.

XX Sequence 16 AA.

Query Match 100.0%; Score 77; DB 19; Length 16;

Best Local Similarity 100.0%; Prod No 0.10-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDPKPKKPKKSPKSS 16

DB 1 DDPKPKKPKKSPKSS 15

RESULT 15

AAV58858

ID AAV58858 standard; Peptide; 16 AA.

XX AAV58858;

XX 08-MAY-2000 (first entry)

XX Membrane binding element used in anti-angiogenic polypeptide.

XX Anti-angiogenic; anti-angiogenic; inhibits membrane binding element;

XX cancer; tumour; therapy.



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Sequence 78, April	Sequence 16, April
Sequence 122, Apr	Sequence 18, April
Sequence 42813, A	Sequence 4, April
Sequence 9, April	Sequence 3, April
Sequence 12, April	Sequence 52, April
Sequence 9, April	Sequence 702, App
Sequence 148, App	Sequence 233, App
Sequence 517, App	Sequence 261, May
Sequence 16617, A	Sequence 261, May
Sequence 16617, A	
Sequence 8, April	
Sequence 5, April	
Sequence 18, April	
Sequence 4, April	
Sequence 3, April	
Sequence 52, April	
Sequence 702, App	
Sequence 233, App	
Sequence 261, May	

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SEQUENCE CHARACTERISTICS:
  LENGTH: 17 amino acids
  TYPE: amino acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  MOLECULE TYPE: peptide
  SEQUENCE DESCRIPTION: SEQ ID NO: 78:
US-09-864-761 78
55.4%; Score 46; DB 9; Length 17;
Query Match 78.9%; Pred. No. 53;
Best Local Similarity 78.9%; Mismatches 1; Indels 0; Gaps 0;
Matches 8; Conservative 7;

QY 3 PNYNYNYKSPK 14
DB 4 PNYNYNYKSPK 15

RESULT 2
US-09-764-864 1122
Sequence 1122; Application US/09/764864
Patent No. US2002012753A1
GENERAL INFORMATION:
  APPLICANT: Posen et al
  TITLE OF INVENTION: Carboxylic Acids, Proteins, and Antibodies
  FILE REFERENCE: PT223
  CURRENT APPLICATION NUMBER: US/09/764,864
  Prior application data removed - consult PALM or file wrapper
  NUMBER OF SEQ ID NOS: 1792
  SOFTWARE: Patent In Ver. 2.0
  SEQ ID NO 1122
  EPOCH: 4aa
  TYPE: PPT
  ORGANISM: Homo sapiens
  FEATURE: SITE
  NAME/KEY: SITE
  LOCAT: 1-64
  OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864 1122
55.4%; Score 46; DB 15; Length 499;
Query Match 72.9%; Pred. No. 53;
Matches 8; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 3 PNYNYNYKSPK 13
DB 222 PNYNYNYKSPK 232

RESULT 3
US-09-864-761-42913
Sequence 42913; Application US/09/864761
Patent No. US20020048763A1
GENERAL INFORMATION:
  APPLICANT: Posen, Sharrin G.
  APPLICANT: Rank, David P.
  APPLICANT: Hanzel, David K.
  APPLICANT: Chen, Wensheng
  TITLE OF INVENTION: HUMAN ANKRD11 SINGLE EXON NUCLEOTIC ACID SEQUENCES USEFUL FOR
  GENE EXPRESSION ANALYSIS BY MICROARRAY
  FILE REFERENCE: America X-1
  CURRENT APPLICATION NUMBER: US/09/864,761
  CURRENT FILING DATE: 2001-05-23
  PRIOR APPLICATION NUMBER: US 60/180,312
  PRIOR FILING DATE: 2000-02-04
  PRIOR APPLICATION NUMBER: US 60/207,456
  PRIOR FILING DATE: 2000-05-26
  PRIOR APPLICATION NUMBER: US 60/632,366
  PRIOR FILING DATE: 2000-04-03
  PRIOR APPLICATION NUMBER: GB 24263.5
  PRIOR FILING DATE: 2000-10-04
  PRIOR APPLICATION NUMBER: US 60/236,359

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PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,587
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/774,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO: 42813
LENGTH: 68
TYPE: PPT
ORGANISM: Homo sapiens
FEATURE:
  OTHER INFORMATION: MAP TO AL035703.17
  OTHER INFORMATION: EXPRESSED IN BRAIN; SIGNAL = 1.1
  OTHER INFORMATION: EXPRESSED IN BONE MARROW; SIGNAL = 1
  OTHER INFORMATION: EXPRESSED IN B14.4; SIGNAL = 1.5
  OTHER INFORMATION: EXPRESSED IN ADULT LIVER; SIGNAL = 1.1
  OTHER INFORMATION: EXPRESSED IN HELA; SIGNAL = 1.2
  OTHER INFORMATION: EXPRESSED IN HELA; SIGNAL = 2.1
  OTHER INFORMATION: EXPRESSED IN PLACENTA; SIGNAL = 1
  OTHER INFORMATION: EST HUMAN HIT: RF76474.2, EVALUATE 3.00e-21
  OTHER INFORMATION: SWISSPROT HIT: P18711, EVALUATE 1.50e-02
US-09-864-761 42813
54.2%; Score 45; DB 10; Length 68;
Query Match 72.7%; Pred. No. 12;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DGYNYNYKSP 11
DB 44 DGYNYNYKSP 54

RESULT 4
US-10-060-763-9
Sequence 9; Application US/10/060763
Publication No. US2003092286A1
GENERAL INFORMATION:
  APPLICANT: Currie, Gary A.J.
  TITLE OF INVENTION: HUMAN ANKRD11 SINGLE EXON NUCLEOTIC ACID SEQUENCES USEFUL FOR
  GENE EXPRESSION ANALYSIS BY MICROARRAY
  FILE REFERENCE: 10147-A
  CURRENT APPLICATION NUMBER: US/10/060,763
  CURRENT FILING DATE: 2002-01-10
  NUMBER OF SEQ ID NOS: 12
  SOFTWARE: Patent In Ver. 2.0
  SEQ ID NO: 9
  LENGTH: 709
  TYPE: PPT
  ORGANISM: Homo sapiens
US-10-060-763-9

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? Sequence 148, Application US/10078770
? Publication No. US20030003471A1
? GENERAL INFORMATION:
? APPLICANT: Fatside, Chertayo O.
? APPLICANT: Forge, Chertaye O.
? APPLICANT: Miao, Guo-Hua
? TITLE OF INVENTION: SHAPE-SENSITIVE POLYMER-CELLULOSE
? FILE REFERENCE: BB-1365 US NA
? CURRENT APPLICATION NUMBER: US/10078770
? CURRENT FILING DATE: 2002-02-19
? PRIOR APPLICATION NUMBER: 65/614,188
? PRIOR FILING DATE: 2000-07-12
? PRIOR APPLICATION NUMBER: 69/143,430
? PRIOR FILING DATE: 1999-07-12
? PRIOR APPLICATION NUMBER: 66/153,534
? PRIOR FILING DATE: 1999-09-13
? PRIOR APPLICATION NUMBER: 66/161,223
? PRIOR FILING DATE: 1999-10-22
? PRIOR APPLICATION NUMBER: 60/159,478
? PRIOR FILING DATE: 1999-10-15
? PRIOR APPLICATION NUMBER: 60/157,401
? PRIOR FILING DATE: 1999-10-01
? PRIOR APPLICATION NUMBER: 66/143,419
? PRIOR FILING DATE: 1999-07-12
? PRIOR APPLICATION NUMBER: 60/143,409
? PRIOR FILING DATE: 1999-07-12
? NUMBER OF SEQ ID NOS: 196
? SOURCE: Microsoft Office 97
? SEQ ID NO 148
? LENGTH: 259
? TYPE: PRT
? ORGANISM: Gryza sativa
? US-10-078-770-148

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Query Match 53.08; Score 44; DB 3; Length 20;
Best Local Similarity 57.18; Prod. No. 53;
Matches 8; Conservative 4; Mismatches 2; Indels

[illegible]

18. SAULTOYAKES 691 96

RESULT 8

US-99-925-302-517
; Sequence 517, Application US/99925302
; Patent No US2002044941A1

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1 TYPE: PRT
2 ORGANISM: Homo sapiens
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4 FEATURE:
5 NAME/KEY: SITE
6 LOCATION: (1)
7 OTHER INFORMATION: Xaa equals any of the naturally occurring L amino acids
8
9 NAME/KEY: SITE
10 LOCATION: (6)
11 OTHER INFORMATION: Xaa equals any of the naturally occurring L amino acids
12
13 NAME/KEY: SITE
14 LOCATION: (23)
15 OTHER INFORMATION: Xaa equals any of the naturally occurring L amino acids

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RESULT 11
112-119-441-446-18


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; SEQ ID NO 3
; LENGTH: 1084
; TYPE: PRT
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (115)
; OTHER INFORMATION: Xaa can be any amino acid
US-10-071-900-3

Query Match      50.6%; Score 42; DP 12; Length 1084;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 3; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 GPRVYVYVSPKSSG 16
   | | | | | | | |
D6 663 GPRVYVYVSPKSSG 883

Search Completed: March 3, 2003, 06:41:38
Job time : 48.0244 secs

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? FILING DATE: 19-JUN-1985
 ? APPLICATION NUMBER: 627,811
 ? FILING DATE: 05-JUL-1984
 ? DEC 10 NO.2.
 ? LENGTH: 142
 5492709-2

Query Match 55.4%, Score 46.5, DB 6, Length 242;

Best Local Similarity 52.4%, Pred. No. 2.7, Mismatches 2, Indels 5, Gaps 1,

QY 1 DGGPPEKK-----SPSKSS 16
 : ||||| :
 Db 104 EGTGKKKKKKKKKKKKKK 124

RESULT 3
 US-08-584-043A-78
 ? Sequence 78, Application US/08584043A
 ? Patent No. 6344436
 ? GENERAL INFORMATION:
 ? APPLICANT: Smith, Louis C.
 ? APPLICANT: Sparrow, James F.
 ? APPLICANT: Hauer, Gochen
 ? APPLICANT: Mins, Martha F.
 ? TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
 ? MAMMOGRAPHY
 ? NUMBER OF SEQUENCES: 133
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Lyon & Lyon
 ? STREET: 633 West Fifth Street
 ? CITY: Los Angeles
 ? STATE: California
 ? COUNTRY: U.S.A.
 ? ZIP: 90071-2066
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 ? COMPUTER: IBM Compatible
 ? OPERATING SYSTEM: IBM PC DOS 6.0
 ? SOFTWARE: WATFORTH 6.1
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/584,043A
 ? FILING DATE: January 8, 1992
 ? CLASSIFICATION: 435
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER:
 ? FILING DATE:
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Warburg, Richard J.
 ? REGISTRATION NUMBER: 11,327
 ? REFERENCE/DOCKET NUMBER: 217/189
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (213) 483-1600
 ? TELEFAX: (213) 955-0440
 ? TELEX: 67-3516
 ? INFORMATION FOR SEQ ID NO. 78:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 17 amino acids
 ? TYPE: amino acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: Peptide
 US-08-584-043A-78

Query Match 55.4%, Score 46, DB 4, Length 17,
 Best Local Similarity 76.9%, Pred. No. 0.76,
 Matches 9, Conservative 0, Mismatches 3, Indels 0, Gaps 0;

QY 3 PKKKKKKSPKSS 14
 : ||||| :
 Db 4 PPKSPKSPKSS 15

RESULT 4
 US-08-492-085B-20
 ? Sequence 20, Application US/08492085B
 ? Patent No. 6018030
 ? GENERAL INFORMATION:
 ? APPLICANT: Ferrari, Franco A.
 ? APPLICANT: Richardson, Charles
 ? APPLICANT: Chambers, James
 ? APPLICANT: Causey, Stuart
 ? APPLICANT: Pollock, Thomas J.
 ? APPLICANT: Cappello, Joseph
 ? APPLICANT: Crissman, John W.
 ? TITLE OF INVENTION: Methods of Administering Particles Containing Epitopes
 ? TITLE OF INVENTION: Methods of Administering Particles Containing Epitopes
 ? NUMBER OF SEQUENCES: 112
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
 ? STREET: Four Embarcadero Center, Suite 3400
 ? CITY: San Francisco
 ? STATE: California
 ? COUNTRY: US
 ? ZIP: 94111
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC DOS/MS DOS
 ? SOFTWARE: PATENT-PROTECTOR #1.0, Version #1.0
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/492,085B
 ? FILING DATE: 07-JUN-1995
 ? CLASSIFICATION: 435
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US 06/927,258
 ? FILING DATE: 04 NOV-1986
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US 07/114,618
 ? FILING DATE: 29-OCT-1987
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US 06/073,849
 ? FILING DATE: 23-APP-1993
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US 08/175,155
 ? FILING DATE: 24-DEC-1993
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Tiscartin, Richard F.
 ? REGISTRATION NUMBER: 31,801
 ? REFERENCE/DOCKET NUMBER: A-5150 EFFECT/MTV
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 415-791-1989
 ? TELEFAX: 415-799-3313
 ? INFORMATION FOR SEQ ID NO. 20:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 285 amino acids
 ? TYPE: amino acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: peptide
 US 08 492 085B 20

Query Match 55.4%, Score 46, DB 3, Length 285;
 Best Local Similarity 90.9%, Pred. No. 12;
 Matches 10, Conservative 0, Mismatches 1, Indels 0, Gaps 0;

QY 4 KKKKKKSPKSS 14
 : ||||| :
 Db 2 PPKKKKSPKSS 73

RESULT 5
 US-08-570-311-4
 ? Sequence 4, Application US/08570311

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TITLE OF INVENTION: Cited Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
GENERATING SYSTEM: PC/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.05
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/58/570,311
FILING DATE: 03/08/1991
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/453,485
FILING DATE: 09-DEC-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-JAN-1991
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/441,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UFI5,03
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-3160
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-570-311-6
Query Match 53.0%; Score 44; DB: Length 350
Best Local Similarity 61.5%; Pred. NO: 29;
Matches 8; Conservative 2; Mismatches 3; Indels 0
Cv 3 PPKKKKSPKSS 15
Db 307 PPKKKKPPASST 319
RESULT 7
US-08-353-485-4
Sequence 4, Application US/08353485
Patent No. 5830710
GENERAL INFORMATION:
APPLICANT: Progulske-Fox, Ann
APPLICANT: Tumwasorn, Somying
APPLICANT: Lepine, Guylaine
APPLICANT: Han, Nairing
APPLICANT: Lantz, Marilyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cited Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL

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#1.0, Version #1.0
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1. *Chlorophyll a* (Chl *a*)

? FILING DATE: 11-DEC-1991
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Deluca Esq., Mark
 ? REGISTRATION NUMBER: 33,229
 ? REFERENCE/DOCKET NUMBER: JCU 1263
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (215) 568-3100
 ? TELEFAX: (215) 568-3439
 ? INFORMATION FOR SEQ ID NO: 31:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 559 amino acids
 ? TYPE: amino acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: protein
 ? PS-SC: 545 9630 31

Query Match 52.4%; Score 43.5; TR 3; Length 100;
Best Local Similarity 61.0%; Pctd. No. 65;
Matches 11; Conservative 1; Mismatches 3; Indels

5. Самодетерминация - вид психического действия, при котором субъект сам определяет свои цели, задачи, содержание деятельности.

291 US 255 (1954)

RESULT 11
PCT-US94-04496-31
; Sequence 31, Application PC/TUS9404496

Query Match	52.48	Score	43.5	DP	5	Length	50
Best Local Similarity	61.18	Pred. No.	45				
Matches	11	Conservative	1	Mismatches	2	Indels	

```

QY 1 DPKK--KKKKSPSKSS 15
| 15 | 1111111111
DB 291 DPKK--KKKKSPSKSS 369

RESULT 12
US-09-072-783-1
; Sequence 1, Application US/08972783
; Patent No. 5849717
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: HUMAN PERLIN BINDING PROTEIN
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Theyte Pharmaceuticals, Inc.
; STREET: 114 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,783
; FILING DATE: Herewith
; CLASSIFICATION: 415
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hillings, Lucy J.
; REGISTRATION NUMBER: 16,749
; REFERENCE/DOCKET NUMBER: FF 0317 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-955-0555
; TELEFAX: 415-945-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 151 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: TESTT02
; CLONE: 2345085
US-09-072-783-1

Query Match 51.8%; Score 42; DB 2; Length 151;
Best Local Similarity 80.0%; Pred. No. 18;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKKKSPSKSS 13
| 1111111111
DE 49 KKKKSPSKSS 59

RESULT 13
US-09-533-669A-18
; Sequence 18, Application US/08972783
; Patent No. 584592
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and BERRY LLP
; STREET: 4300 Columbia Center, 701 Fifth Avenue

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; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08972783
; FILING DATE: 22-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark, David J.
; REGISTRATION NUMBER: 31,902
; REFERENCE/DOCKET NUMBER: 210421420
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206 622-4900
; TELEFAX: 206 682-6031
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 732 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-533-669A-18

Query Match 51.8%; Score 43; DB 4; Length 732;
Best Local Similarity 79.2%; Pred. No. 84;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DPKK--KKKKSPSKSS 13
| 1111111111
DE 271 DPKK--KKKKSPSKSS 283

RESULT 14
US-09-307-143-4
; Sequence 4, Application US/09007143
; Patent No. 635157
; GENERAL INFORMATION:
; APPLICANT: Gonzalez C.
; APPLICANT: Lange, B.
; TITLE OF INVENTION: METHODS BASED ON LOCALIZATION OF HSP90 TO THE
; FILE REFERENCE: 9882-003
; CURRENT APPLICATION NUMBER: US/09/307,143
; CURRENT FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 732
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-307-143-4

Query Match 51.8%; Score 43; DB 4; Length 732;
Best Local Similarity 79.2%; Pred. No. 84;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DPKK--KKKKSPSKSS 13
| 1111111111
DE 271 DPKK--KKKKSPSKSS 283

RESULT 15
US-09-183-861-18
; Sequence 18, Application US/09007143
; Patent No. 635155
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Corixa Corp., Antonio

```







```

OX NCBI_TaxID=10090;
RN [1]
PP SEQUENCE FROM N.A. AND CHAPA-TEPICATION;
PC TISSUE-Testis;
RA MEDLINE-9926011, PubMed1011617,
RX Ruas F.W., Lee K., Edelhoff S., Diserche C., Braun P.E.;
RT "Cloning and characterization of the mouse interleukin enhancer
binding factor 3 (Ilf3) homolog in a screen for PNA binding
proteins";
RL Mamm Genome 10:451-456(1999)
CC -- FUNCTION: May facilitate double stranded PNA-regulated gene
expression at the level of post-transcription. Can act as a
translation inhibitory protein which binds to coding sequences of
acid beta-glucosidase (GCase) and other mRNAs and functions at the
initiation phase of GCase mRNA translation, probably by inhibiting
its binding to poly-A. Can regulate protein arginine N-
methyltransferase 1 activity (By similarity).
CC -- SUBUNIT: Interacts with PMS and SMN proteins and also with
HMT112 (By similarity).
CC -- SUBCELLULAR LOCATION: Nuclear.
CC -- TISSUE SPECIFICITY: Ubiquitous. Expressed at high levels in the
thymus, testis, ovary and at lower levels in the spleen.
CC -- PTM: Phosphorylated by RNA-dependent protein kinase (PRKF) (By
similarity).
CC -- PTM: Methylated by protein arginine N-methyltransferase 1 (By
similarity).
CC -- SIMILARITY: CONTAINS 5 DPM (DPM-1) REPEAT (PNA BINDING) DOMAINS.
CC
CC THE SWISS-PROT entry is copyright. It is provided through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL database.
CC The European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement. (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch.)
CC
DP FMBP; AF069467, AAC71002.1;
DR MG0; MG11339973; 11f3;
DR InterPro; IPR001159; DS_PRO;
DR Pfam; PF00015; dsrm_2;
DR SMART; SMART00358; DSFM; 2;
DR PROSITE; PS00137; DS_PBD; 2;
KW Transcriptional regulation, PNA binding, PNA binding, Nuclear protein,
Repeat, Phosphorylation, Methylation
FT DOMAIN 344 402
DI DIAPYRITE NUCLEAP LOCALIZATION SIGNAL
(POTENTIAL)
FT DOMAIN 411 480
DPM 1;
FT DOMAIN 537 603
DPM 2;
FT DOMAIN 620 672
INTERACTS WITH HPM1112 (By similarity);
FT DOMAIN 653 672
ARG/GLY-RICH;
FT DOMAIN 11 15
POLY-ARG;
FT DOMAIN 368 402
POLY-LYS;
FT DOMAIN 647 650
POLY-PRO;
FT DOMAIN 714 723
POLY-GLY;
FT DOMAIN 810 813
POLY-GLY;
SQ SEQUENCE 311 AA, 37441 MW, 5.7749875596183 kDa;
Query Match 61.4%; Score 51; PP 1; Length 911;
Best Local Similarity 83.3%; Pred. No. 4.6;
Matches 10; Conservative 0, Mismatches 6, Gaps 0.
QY : GGGGSGGGGGG 10
DB 34: GGGGSGGGGGG 402
RESULT 5
ID H13_RABIT STANFORD, FFT, 312 AA.
AC P08111;
DT 21 JUN 1998 (Seq 01, Created)
ET 21 JUN 1998 (Seq 01, Last sequence update)
DT 15-JUN-1999 (Seq 19, Last annotation update)

```

```

DE Histone H1.3
OS Oryctolagus cuniculus (Rabbit)
OC Eukaryota; Metazoa; Chordata; Mammalia; Vertebrata; Eukaryota;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
CX NCBI_TaxID=9986;
RN [1]
PP SEQUENCE
RA Hsiang M., Laryman C.P., Cole P.D.;
PC Unpublished results, cited by.
RL Cole P.D.;
FL (In) TSO P.O.F. (eds.);
PL The molecular biology of the mammalian genetic apparatus, pp 1-03 104,
Elsevier, Amsterdam (1977)
RN [2]
PP SEQUENCE OF 1-72
EX VEFNINR77068710; PubMed 6167370;
RA Pall S.C., Cole P.D.;
FL "Amino acid sequence and sequence variability of the amino-terminal
regions of lysine-rich histones.";
EL J. Biol. Chem. 246:7175-7190(1971).
RN [3]
PP SEQUENCE OF 73-107
EX MEDLINE74141498; PubMed4822503;
RA Jones G.M.T., Pall S.C., Cole P.D.;
FL "Extension of the amino acid sequence of a lysine-rich histone.";
PL J. Biol. Chem. 249:2649-2653(1974).
CC -- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF
NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
CC -- SUBCELLULAR LOCATION: Nuclear.
CC -- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY
PIR; A02579; HSPR13
DR PEST; P08497; ICR3;
DR InterPro; IPR001366; Histone_H1/H5;
DR Pfam; PF00538; linker_histone_1;
DR ProDom; PD000373; linkerhist_N; 1;
DR SMART; SM00525; H1s; 1;
KW Chromosomal protein, Nuclear protein, DNA binding, Multigene family;
FT MOD_RES 1 1 ACETYLATION.
FT DOMAIN 47 110 GLIOTAP;
SQ SEQUENCE 213 AA, 23415 MW, 4.55483615445 kDa;
Query Match 60.7%; Score 50; PP 1; Length 213;
Best Local Similarity 89.4%; Pred. No. 1.6;
Matches 11; Conservative 0, Mismatches 1, Indels 0, Gaps 1;
QY : SSKPSKPKPKV KPKS 15
DB 12 AKESPAKFFFAKFFS 28
RESULT 6
ID PARV CAEEL STANDARD, FFT, 375 AA.
AC A01678;
DT 15 JUN 2002 (Seq 41, Created)
DT 15-JUN-2002 (Seq 41, Last sequence update)
DT 15 JUN 2002 (Seq 41, Last annotation update)
DE Parvulin-like protein.
GN P01012.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Elasmobranchia; Phabidida; Phabididae;
OC Phabididae; Pelodermata; Caenorhabditis.
CX NCBI_TaxID=6239;
RN [1]
PP SEQUENCE FROM N.A.
RC STRAIN= Bristol N2;
RA Woessner J.;
EL Submitted (JUL-1997) to the EMBL/GenBank/CCP databases.
CC -- FUNCTION: Probably plays a role in the regulation of cell division
and cytoskeleton organization (By similarity).
CC -- SUBCELLULAR LOCATION: Cytoplasmic, localized to focal adhesions
(By similarity).
CC

```



```

DB 120 KPSKYYKYPG 131
[1] [1111] [11]
ID PTHR RABIT STANDARD; PRT: 177 AA.
AC Q2GUC7,
DT 16-OCT-2001 (rel. 40, Created)
DT 16-OCT-2001 (rel. 40, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE Parathyroid hormone-related protein precursor (PTH rP) (PTHrP)
DE (PTHrP)
GN PTHrP OR PTHRP.
CC "This is a human PTHrP."
CC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
CC Mammalia, Eutheria, Lagomorpha, Leporidae, Cytodactylus.
CC NCBI TaxID 9986.
[1]
RN SEQUENCE FROM N.A.
RA McQuibban-Carlson J.F., Minick M., Emanuel J.P., Iwerczyk S.J.;
RT "Cloning and expression of rabbit parathyroid hormone-related
RT protein."
RL PubMed 7474747.
CC - FUNCTION: PLAYS A PHYSIOLOGICAL ROLE IN LACTATION, POSSIBLY AS A
CC HORMONE FOR THE MOBILIZATION AND/OR TRANSFER OF CALCIUM TO THE
CC MILK.
CC - SUBCELLULAR LOCATION: Secreted.
CC - SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announcement/
CC or send an email to license@sib-sib.ch).
CC
CC EMBL: AF300703, MAG13414.1, -.
CC DDB: H3272, IBCG.
CC RefSeq: NP000426; PTH related.
CC Pfam: PF001415; Parathyroid_hrm.
CC ProDom: PD013225; PTH related; 1.
CC SMART: SM00087; PTH, 1.
CC PROSITE: PS00435; PAPATHYROID; 1.
CC CATH: 3.40.130.10; PTH-related.
CC SIGNAL: 1, 24 POTENTIAL.
CC PROPEP: 25, 34 BY SIMILARITY.
CC PTH CHAIN: 37, 177 PAPATHYROID HORMONE-RELATED PROTEIN.
CC SEQUENCE: 177 AA; 20005 MW; E4D9F427657E19 CDS;
CC
CC Query Match: 59.0%; Score 49; DB 1; Length 177;
CC Best Local Similarity: 76.0%; Pred. No 18;
CC Matches: 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 4 KPSKYYKYPG 15
DB 120 KPSKYYKYPG 131
[1] [1111] [11]
ID PTHR RAT STANDARD; PRT: 177 AA.
AC P13085;
DT 01-JAN-1990 (rel. 13, Created)
DT 01-JAN-1990 (rel. 13, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE Parathyroid hormone-related protein precursor (PTH rP) (PTHrP) (Rat)
DE PTHrP OR PTHRP.
CC "Parathyroid hormone-related protein (PTHrP) is a secreted protein that
CC plays a role in bone metabolism."
CC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
CC Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus

```


KW Cytoskeleton, Membrane, Calmodulin-binding, Phosphorylation;
 KW Alternative splicing.
 FT DCMAIN 684 701 CALMODULIN-BINDING (POTENTIAL).
 FT MCD.RES 683 683 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
 FT VARSPLIC 576 607 MISSING (IN ISOFORM 1).
 FT CCNELICT 49 50 EN -> SS (IN REF. 1).
 FT CCNELICT 50 50 Q -> R (IN REF. 1).
 FT CCNELICT 362 362 Q -> P (IN REF. 2).
 FT CCNELICT 420 420 V -> M (IN REF. 2).
 FT CCNELICT 421 421 F -> L (IN REF. 1).
 FT CCNELICT 424 433 KIMAROO -> CHISTONK (IN REF. 2).
 FT CCNELICT 484 484 K -> Q (IN REF. 2).
 SQ SEQUENCE 706 AA; 79154 MW; EB86AP502A4L/B41 CPO64;
 Query Match 59.0%; Score 49; DB 1; Length 706;
 Best Local Similarity 100.0%; Pred. No. 7;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 3 SKSPSKKKK 12
 Db 679 SKSPSKKKK 698

Search completed: March 3, 2003, 06:36:19
 Job time : 7.65854 secs


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AC Q91550;
LT 01-NOV-1996 (TrEMBLrel 01, Created)
DT 01-NOV-1996 (TrEMBLrel 01, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel 19, Last annotation update)
DE dsRNA-binding protein 4P.1.
OS Xenopus laevis (African clawed frog)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenocephalidae; Xenopus
OX NCBI_TaxID=8355;
RN [1]
RF SEQUENCE FROM N.A.
RC MEDLINE=95066448; PubMed=7422119;
RA Bass B.D., Hurst S.R., Singer J.D.;
RT "Binding properties of newly identified Xenopus proteins containing
RT dsRNA binding motifs."
RL Curr Biol 4 301 314(1994).
DE EMBL: M67155, AAA19960.1; -
DR InterPro: IPR001159; DS_PBD.
DR Pfam: PF00060; DSRM_2.
DR SMART: SM00358; DSRM_2.
DR PROSITE: PS00137, PS_PBD, 2
DR NCBI-TER 1
SQ SEQUENCE 896 AA, 7690 MW, E26463AP716E1326 QPC64;

Query Match 61.4%; Score 51; DB 13; Length 895;
Best Local Similarity 83.3%; Pred. No. 5.9;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GSSKSPSKKKK 12
DB 373 GDSKSPSKKKK 100

RESULT 3
Q91551 PRELIMINARY; PRT: 800 AA.
ID Q91551;
AC Q91551;
DT 01-NOV-1996 (TrEMBLrel 01, Created)
DI 01-NOV-1996 (TrEMBLrel 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel 19, Last annotation update)
DE dsRNA-binding protein 4P.2 (Fragment).
OS Xenopus laevis (African clawed frog)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenocephalidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RF SEQUENCE FROM N.A.
RC TISSUE=OVARY.
RA Bass B.D., Hurst S.R., Singer J.D.;
RT "Binding properties of newly identified Xenopus proteins containing
RT dsRNA binding motifs."
RL Curr Biol 4 301 314(1994).
DE EMBL: M67156, AAA19961.1; -
DR HEGP: P35159; 1STU.
DR InterPro: IPR001159; DS_RBD.
DR Pfam: PF00060; DSRM_2.
DR SMART: SM00358; DSRM_2.
DR PROSITE: PS00137, PS_PBD, 2
DR NCBI-TER 1
SQ SEQUENCE 896 AA, 8750 MW, C210051PAP17F1R QPC64;

Query Match 61.4%; Score 51; DB 13; Length 800;
Best Local Similarity 83.3%; Pred. No. 6.2;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GSSKSPSKKKK 12
DB 373 GDSKSPSKKKK 100

RESULT 4
Q9DEU4 PRELIMINARY; PRT: 896 AA.
ID Q9DEU4;
AC Q9DEU4;
DT 01-MAR-2001 (TrEMBLrel 16, Created)
DI 01-MAR-2001 (TrEMBLrel 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel 19, Last annotation update)
DE CCAAT box transcription factor p122 subunit.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenocephalidae; Xenopus
OX NCBI_TaxID=8355;
RN [1]
RF SEQUENCE FROM N.A.
RC MEDLINE=7435367; PubMed 10900122;
RA Blaszkowski J., Robinson C., Orford P., Elgar S., Scariett G.,
RA Peterkin T., Malaitte M., Kneale G., Worthington M., Guille M.;
RT "RNA-dependent cytoplasmic anchoring of a transcription factor subunit
RT during Xenopus development."
RL EMBL: J193683 3693(2000).
DR EMBO J 19 3683 3693(2000).
DR EMBL: AF042249.1; -
DR InterPro: IPR001159; DS_PBD.
DR Pfam: PF00060; DSRM_2.
DR SMART: SM00358; DSRM_2.
DR PROSITE: PS00137, PS_PBD, 2
DR NCBI-TER 1
SQ SEQUENCE 896 AA, 7960 MW, P86P4047PAP4A1 QPC64;

Query Match 61.4%; Score 51; DB 13; Length 896;
Best Local Similarity 83.3%; Pred. No. 6.9;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GSSKSPSKKKK 12
DB 373 GDSKSPSKKKK 100

RESULT 5
Q9TD10 PRELIMINARY; PRT: 1954 AA.
ID Q9TD10;
AC Q9TD10;
DT 01-JUN-2000 (TrEMBLrel 21, Created)
DI 01-JUN-2000 (TrEMBLrel 21, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel 21, Last annotation update)
DE Chromodomain helicase DNA binding Protein 5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RF SEQUENCE FROM N.A.
RA Thompson P.M., Gutch T., White P.S., Brodeur G.M.;
RT "CHD5, a new Member of the Chromodomain Gene Family, is Preferentially
RT Expressed in the Nervous System."
RL Submitted (SEP 2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF425231, AA199602.1; -
DR Helicase
SQ SEQUENCE 1954 AA, 203048 MW, E333062B5B55E71F QPC64;

Query Match 61.4%; Score 51; DB 4; Length 1954;
Best Local Similarity 69.8%; Pred. No. 14;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GSSKSPSKKKK 16
DB 373 GDSKSPSKKKK 105

RESULT 6
Q9C2J9 PRELIMINARY; PRT: 2095 AA.
ID Q9C2J9

```



```

Submitted (MAR-2006) to the EMBL/GenBank/DBJ databases.
[4]
SEQUENCE FROM N.A.
EU Arabidopsis sequencing project.
Submitted (MAR-2006) to the EMBL/GenBank/DBJ databases.
EMBL; AL079350; CAB4512.1; -.
EMBL; AL161563; CAB81345.1; -.
HSP; Q06648; IPEK
InterPro: IP2001179; FKBP_PPIase
Pfam: PF00754; FKBP_1
PROSITE: PS00454; FKBP_PPIASE_2, 1.
PROSITE: PS00059; FKBP_PPIASE_3, 1.
Hypothetical protein
SEQUENCE 487 AA, 53292 MW, 583FACTG7AG-CAAC-25934.

Query Match 59.0%, Score 49, DB 11, Length 497;
Best Local Similarity 52.2%, Field No. 5,7;
Matches 15, Conservative 1, Mismatches 2, Indels 9, Gaps 1;

QY 2 SRSPEK-----KFKFKPG 16
||| ||| ||| ||| |||
DE 210 SPTTSTSAEYFNFFKFFKPG 162

RESULT 10
Q924X4 PRELIMINARY; PRT; 175 AA.
Q924X4
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Parathyroid hormone-related protein precursor.
PHLH.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Primata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus.
NCPI_TaxID=10089;
[1]
SEQUENCE FROM N.A.
STRAIN=C3H/HEJ; TISSUE=LUNG;
Manenti G., Peisssel B., Gariboldi M., Falvella F.S., Zaffaroni D.,
Covelli V., Sarau A., Diagani T.A.;
" A cancer modifier role for parathyroid hormone related protein." ;
Submitted (MAY-2006) to the EMBL/GenBank/DBJ databases.
EMBL; AC278132; CAB29218.1.
InterPro: IP001413; Parathyrd hrm.
InterPro: IP001626; PTH related.
Pfam: PF01279, Parathyroid3, 1.
ProDom: PD01325, PTH related, 1.
PROSITE: PS00335, PARATHYR-10, PTHFR-1.
Signal.
KW SIGNAL.
FT SIGNAL 1 36 POTENTIAL
FT CHAIN 37 175 PARATHYROID HORMONE-RELATED PROTEIN.
SEQUENCE 175 AA, 20046 MW, 40256P-21130834= Q924X4,

Query Match 59.0%, Score 49; DB 11; Length 175;
Best Local Similarity 75.0%, Field No. 3,2;
Matches 9, Conservative 1, Mismatches 2, Indels 0, Gaps 0;

QY 4 KPSKPKKPKKPG 15
||| ||| ||| |||
DB 120 KPSKPKKPKKPG 131

RESULT 11
Q980Z3 PRELIMINARY; PRT; 202 AA.
Q980Z3
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Parathyroid hormone-related protein.
Proteinaceous vesiculus (protein)

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Query Match 59.3%; Score 49; PR 10; Length 100;
Best Local Similarity 75.0%; Pred. No. 9.9;
Matches 9; Conservative 1; Mismatches 2; Indels 1; Gaps 0;

US-09-897-778-165

Query Match 59.3%; Score 49; PR 10; Length 100;
Best Local Similarity 75.0%; Pred. No. 9.9;
Matches 9; Conservative 1; Mismatches 2; Indels 1; Gaps 0;

US-09-897-778-165

US-09-897-778-165

Query Match 59.3%; Score 49; PR 10; Length 100;
Best Local Similarity 75.0%; Pred. No. 9.9;
Matches 9; Conservative 1; Mismatches 2; Indels 1; Gaps 0;

US-09-897-778-165

US-09-897-778-165

Query Match 59.3%; Score 49; PR 10; Length 100;
Best Local Similarity 75.0%; Pred. No. 9.9;
Matches 9; Conservative 1; Mismatches 2; Indels 1; Gaps 0;

US-09-897-778-165

US-09-897-778-165

Query Match 59.3%; Score 49; PR 10; Length 100;
Best Local Similarity 75.0%; Pred. No. 9.9;
Matches 9; Conservative 1; Mismatches 2; Indels 1; Gaps 0;

US-09-897-778-165

Query Match 59.3%; Score 49; PR 10; Length 100;
Best Local Similarity 75.0%; Pred. No. 9.9;
Matches 9; Conservative 1; Mismatches 2; Indels 1; Gaps 0;

US-09-897-778-165

Query Match 59.3%; Score 49; PR 10; Length 100;
Best Local Similarity 75.0%; Pred. No. 9.9;
Matches 9; Conservative 1; Mismatches 2; Indels 1; Gaps 0;

US-09-897-778-165

US-09-897-778-165

US-09-897-778-165

US-09-897-778-165

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US-09-897-778-165

US-09-897-778-165

US-09-897-778-165

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; SEQ ID NO 2
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-058-820 2

Query Match 57.8%; Score 48; DB 9; Length 473;
Best Local Similarity 57.1%; Pred. No. 32;
Matches 12, Conservative 1, Mismatches 2, Indels 6, Gaps 1,

QY 2 SQKS FSKFKFKPKD 16
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DB 207 SSKSKFKSKSKFKFKFKSK 232

RESULT 10
US-10-058-820 1
; Sequence 1, Application US/10358820
; Patent No. US599015C479A1
; GENERAL INFORMATION
; APPLICANT: Regeneron, Jonathan S.
; APPLICANT: Bodish, Harvey F.
; TITLE OF INVENTION: Expression Cloning Method
; FILE REFERENCE: 600 2028 002
; CURRENT APPLICATION NUMBER: US/10/058,820
; PRIOR FILING DATE: 2002 06 17
; PRIOR APPLICATION NUMBER: US 60/125,551
; PRIOR FILING DATE: 2001 09 26
; PRIOR APPLICATION NUMBER: US 60/298,963
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/284,816
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-058-820-1

Query Match 57.8%; Score 48; DB 9; Length 473;
Best Local Similarity 57.1%; Pred. No. 32;
Matches 12, Conservative 1, Mismatches 2, Indels 6, Gaps 1;

QY 2 SQKS FSKFKFKPKD 16
||| ||| ||| |||
DB 207 SSKSKFKSKSKFKFKFKSK 232

RESULT 11
US 09 064 864 1122
; Sequence 1122, Application US/0904864
; Patent No. US6009013279A1
; GENERAL INFORMATION
; APPLICANT: Posen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: 67223
; CURRENT APPLICATION NUMBER: US/09/064,864
; PRIOR FILING DATE: 2001 01 17
; PRIOR APPLICATION NUMBER: US 60/117,474
; NUMBER OF SEQ ID NOS: 1797
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1122
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 191
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-064-864-1122

Query Match 55.4%; Score 46; DB 10; Length 498;
Best Local Similarity 53.3%; Pred. No. 136402;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 KSPSKSKSKSKPKD 16
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DB 220 KSKSKSKSKSKSKSKSK 232

RESULT 12
US-09-870-122-1
; Sequence 1, Application US/090870122
; Patent No. US6000142009A1
; GENERAL INFORMATION
; APPLICANT: Regents of the University of Minnesota et al.
; TITLE OF INVENTION: Streptococcal C5a Peptide Vaccine
; FILE REFERENCE: 600 450001
; CURRENT APPLICATION NUMBER: US/09/370,122
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: US 09/206,898
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: US 08/593,075
; PRIOR FILING DATE: 1996 01 22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1164
; TYPE: PPT
; ORGANISM: Streptococcus pyogenes
US-09-870-122-1

Query Match 55.4%; Score 46; DB 10; Length 1164;
Best Local Similarity 53.3%; Pred. No. 136402;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 GSKSKSKSKSKSKSKPKD 15
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DB 1056 GSKSKSKSKSKSKSKSKPKD 1070

RESULT 13
US 09 064 864 858
; Sequence 858, Application US/0906858
; Patent No. US6000044941A1
; GENERAL INFORMATION
; APPLICANT: Posen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: 60104
; CURRENT APPLICATION NUMBER: US/09/068,858
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US99/05618
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/104,070
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 858
; LENGTH: 58
; TYPE: PPT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US 09 064 864 858
; LOCATION: (17)
; NAME/KEY: SITE
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US 09 064 864 858
; LOCATION: (19)
; NAME/KEY: SITE
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US 09 064 864 858
; LOCATION: (42)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US 09 064 864 858
; NAME/KEY: SITE

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Version 5.1.3
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Without alignment: 46.138 Million bits/sec

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Patent No. 5217896
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US-08-411-726-5
Sequence 5, App11-110 US/08411726
Patent No. 5880093
GENERAL INFORMATION:
APPLICANT: BAGNOLI, Franco
TITLE OF INVENTION: Use of Parathion, Its Biologically
Active Fragments and Correlated Popitides, for the Preparation
of Pharmaceutical Compositions Useful for the Treatment of
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Kenyon & Kenyon
STREET: 1 Broadway
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.2
SOFTWARE: WordPerfect 6.1 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/411,726
FILING DATE: 05-APR-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/02765
FILING DATE: 09-OCT-1993
APPLICATION NUMBER: MI 92A002331
FILING DATE: 09-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: PALMESE, Maria Luisa
REGISTRATION NUMBER: 34,402
REFERENCE/KEYWORD NUMBER: C111,0300
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 422 7200
TELEFAX: 212-425-5288
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US 08-411-726-5

ALIGNMENTS

RESULT 1
US-08-411-726-5
Sequence 5, App11-110 US/08411726
Patent No. 5880093
GENERAL INFORMATION:
APPLICANT: BAGNOLI, Franco
TITLE OF INVENTION: Use of Parathion, Its Biologically
Active Fragments and Correlated Popitides, for the Preparation
of Pharmaceutical Compositions Useful for the Treatment of
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Kenyon & Kenyon
STREET: 1 Broadway
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10004
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.2
SOFTWARE: WordPerfect 6.1 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/411,726
FILING DATE: 05-APR-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/02765
FILING DATE: 09-OCT-1993
APPLICATION NUMBER: MI 92A002331
FILING DATE: 09-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: PALMESE, Maria Luisa
REGISTRATION NUMBER: 34,402
REFERENCE/KEYWORD NUMBER: C111,0300
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 422 7200
TELEFAX: 212-425-5288
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US 08-411-726-5
Query Match 59.0% Score 47.0 Length 141
Best Local Similarity 59.0% Score 47.0 Length 141
Matches 9, Conservative 1, Mismatches 0, Indels 0, Gaps 0

Query Match 59.01; Score 49; DB 4; Length 1617;
Best Local Similarity 66.78; Pred. No. 45;
Matches 10; Conservative 1; Mismatches 4; Indels 7; Gaps 7;

Query Match 55.18; Score 46; DB 4; Length 1164;
Best Local Similarity 53.38; Pred. No. 75;
Matches 8; Conservative 3; Mismatches 4; Indels 7; Gaps 7;

Query Match 55.18; Score 46; DB 4; Length 1164;
Best Local Similarity 53.38; Pred. No. 75;
Matches 8; Conservative 3; Mismatches 4; Indels 7; Gaps 7;

Query Match 55.18; Score 46; DB 4; Length 1164;
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Best Local Similarity 53.38; Pred. No. 75;
Matches 8; Conservative 3; Mismatches 4; Indels 7; Gaps 7;

Query Match 55.18; Score 46; DB 4; Length 1164;
Best Local Similarity 53.38; Pred. No. 75;
Matches 8; Conservative 3; Mismatches 4; Indels 7; Gaps 7;

Query Match 55.18; Score 46; DB 4; Length 1164;
Best Local Similarity 53.38; Pred. No. 75;
Matches 8; Conservative 3; Mismatches 4; Indels 7; Gaps 7;

Query Match 55.18; Score 46; DB 4; Length 1164;
Best Local Similarity 53.38; Pred. No. 75;
Matches 8; Conservative 3; Mismatches 4; Indels 7; Gaps 7;

Query Match 55.18; Score 46; DB 4; Length 1164;
Best Local Similarity 53.38; Pred. No. 75;
Matches 8; Conservative 3; Mismatches 4; Indels 7; Gaps 7;

Query Match 55.18; Score 46; DB 4; Length 1164;
Best Local Similarity 53.38; Pred. No. 75;
Matches 8; Conservative 3; Mismatches 4; Indels 7; Gaps 7;

Query Match 55.18; Score 46; DB 4; Length 1164;
Best Local Similarity 53.38; Pred. No. 75;
Matches 8; Conservative 3; Mismatches 4; Indels 7; Gaps 7;

Query Match 55.18; Score 46; DB 4; Length 1164;
Best Local Similarity 53.38; Pred. No. 75;
Matches 8; Conservative 3; Mismatches 4; Indels 7; Gaps 7;

Query Match 55.18; Score 46; DB 4; Length 1164;
Best Local Similarity 53.38; Pred. No. 75;
Matches 8; Conservative 3; Mismatches 4; Indels 7; Gaps 7;

DB 1056 GSCQAKRERETP3 1073

RESULT 10

US-09-206-898-1
 ? Sequence 1, Application: US/00000000
 ? Patent No. 635025
 ? GENERAL INFORMATION:
 ? APPLICANT: Cleary, Paul P.
 ? APPLICANT: Staflin, Deborah K.
 ? TITLE OF INVENTION: STREPTOCOCCAL C3a RECEPTOR WARMING
 ? FILE REFERENCE: 600.450051
 ? CURRENT APPLICATION NUMBER: US/09/206,898
 ? CURRENT FILING DATE: 1998 12 07
 ? NUMBER OF SEQ ID NOS: 23
 ? SOFTWARE: SeqSeq for Windows Version 2.0
 ? SEQ ID NO 1
 ? TYPE: PRT
 ? LENGTH: 1164
 ? ORGANISM: Streptococcus pyogenes
 US-09-206-898-1

Query Match 53.03, Score 44, PP 4, Length 104;
 Best Local Similarity 53.03, Pct 75,
 Matches 6, Conservative 1, Mismatches 4, Indels 6, Gaps 0.

CY 1 GSCQAKRERETP3 1073

DB 1056 GSCQAKRERETP3 1073

RESULT 11

US-09-039-780A-10
 ? Sequence 10, Application: US/00000000
 ? Patent No. 6376248
 ? GENERAL INFORMATION:
 ? APPLICANT: HAWLEY NELSON, PAMELA
 ? INVENTOR: LAM, JIANJING
 ? SHIH, POJEN
 ? JESSE, JOEL A.
 ? SCHIFFERLI, KEVIN P.
 ? GREYERH, GUILLOT
 ? TITLE OF INVENTION: PEPTIDE ENHANCED TRANSCRIPTION
 ? NUMBER OF SEQUENCES: 120
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: GREENLEE, WINNER & SULLIVAN
 ? STREET: 6370 MANHATTAN CIRCLE, SUITE 201
 ? CITY: BOULDER
 ? STATE: CO
 ? COUNTRY: US
 ? ZIP: 80103
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC Compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patent In Release #1.0, Version #1.30
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/09/039,780A
 ? FILING DATE: 16 Mar 1998
 ? CLASSIFICATION: Unknown
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: SULLIVAN, SALLY A.
 ? REGISTRATION NUMBER: 32,064
 ? REFERENCE/PROFIT NUMBER: 00 sec
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (303)499-8080
 ? TELEFAX: (303)499-8089
 ? INFORMATION FOR SEQ ID NO: 1:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 16 amino acids
 ? TYPE: amino acid
 ? STRANDEDNESS: not relevant
 ? TOPOLOGY: linear
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC Compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patent In Release #1.0, Version #1.30
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/09/039,780A
 ? FILING DATE: 16 Mar 1998
 ? CLASSIFICATION: Unknown
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: SULLIVAN, SALLY A.
 ? REGISTRATION NUMBER: 32,064
 ? REFERENCE/PROFIT NUMBER: 00 sec
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (303)499-8080
 ? TELEFAX: (303)499-8089
 ? INFORMATION FOR SEQ ID NO: 1:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 16 amino acids
 ? TYPE: amino acid
 ? STRANDEDNESS: not relevant
 ? TOPOLOGY: linear

MOLECULE TYPE: PRT
 SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 US-09-039-780A-10

Query Match 53.03, Score 44, PP 4, Length 19;
 Best Local Similarity 53.03, Pct 31;
 Matches 6, Conservative 1, Mismatches 4, Indels 0, Gaps 0.

CY 4 KPSKPKKPKPKPKD 16

DB 11 KPSKPKKPKPKPKD 23

RESULT 12

US-09-039-780A-9
 ? Sequence 9, Application: US/00000000
 ? Patent No. 6376248
 ? GENERAL INFORMATION:
 ? APPLICANT: HAWLEY NELSON, PAMELA
 ? INVENTOR: LAM, JIANJING
 ? SHIH, POJEN
 ? JESSE, JOEL A.
 ? SCHIFFERLI, KEVIN P.
 ? GREYERH, GUILLOT
 ? TITLE OF INVENTION: PEPTIDE ENHANCED TRANSCRIPTIONS
 ? NUMBER OF SEQUENCES: 120
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: GREENLEE, WINNER & SULLIVAN
 ? STREET: 6370 MANHATTAN CIRCLE, SUITE 201
 ? CITY: BOULDER
 ? STATE: CO
 ? COUNTRY: US
 ? ZIP: 80103
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC Compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patent In Release #1.0, Version #1.30
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/09/039,780A
 ? FILING DATE: 16 Mar 1998
 ? CLASSIFICATION: Unknown
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: SULLIVAN, SALLY A.
 ? REGISTRATION NUMBER: 32,064
 ? REFERENCE/PROFIT NUMBER: 00 sec
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (303)499-8080
 ? TELEFAX: (303)499-8089
 ? INFORMATION FOR SEQ ID NO: 9:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 23 amino acids
 ? TYPE: amino acid
 ? STRANDEDNESS: not relevant
 ? TOPOLOGY: linear
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC Compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patent In Release #1.0, Version #1.30
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/09/039,780A
 ? FILING DATE: 16 Mar 1998
 ? CLASSIFICATION: Unknown
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: SULLIVAN, SALLY A.
 ? REGISTRATION NUMBER: 32,064
 ? REFERENCE/PROFIT NUMBER: 00 sec
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (303)499-8080
 ? TELEFAX: (303)499-8089
 ? INFORMATION FOR SEQ ID NO: 9:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 23 amino acids
 ? TYPE: amino acid
 ? STRANDEDNESS: not relevant
 ? TOPOLOGY: linear

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Best Local Similarity 53.03, Pct 37;

Matches 6, Conservative 0, Mismatches 4, Indels 0, Gaps 0.

CY 4 KPSKPKKPKPKPKD 16

DB 11 KPSKPKKPKPKPKD 23

Job time : 19.3415 secs

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Seq. No. 17;
Mismatches 7; Indels 2; Gaps 1;

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Mismatches 7; Indels 2; Gaps 1;

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Mismatches 7; Indels 2; Gaps 1;

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Seq. No. 17;
Mismatches 7; Indels 2; Gaps 1;

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Seq. No. 17;
Mismatches 7; Indels 2; Gaps 1;

DB 49; DB 2; Local: 1000;
Seq. No. 17;
Mismatches 7; Indels 2; Gaps 1;

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Seq. No. 17;
Mismatches 7; Indels 2; Gaps 1;

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Seq. No. 17;
Mismatches 7; Indels 2; Gaps 1;

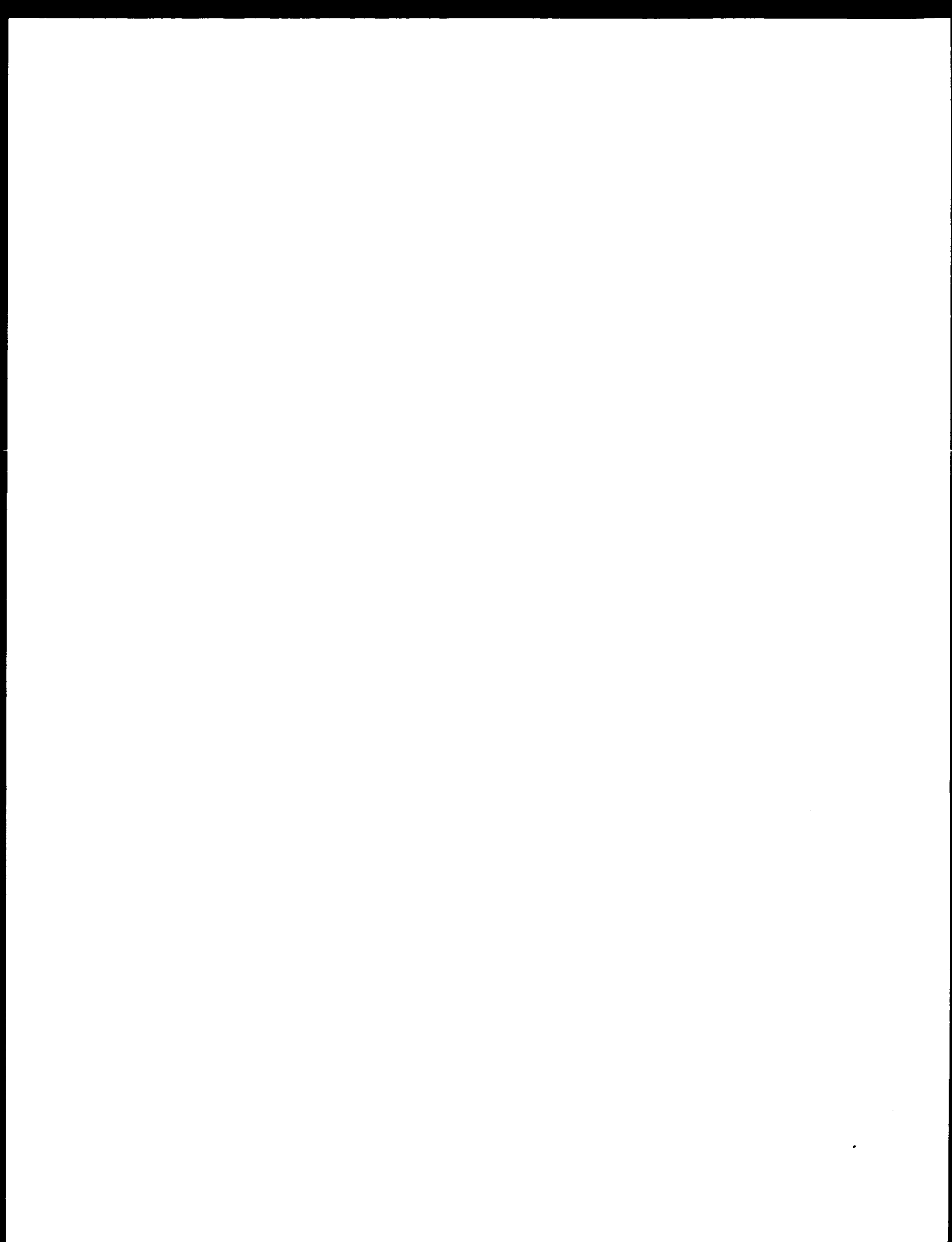
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Seq. No. 17;
Mismatches 7; Indels 2; Gaps 1;

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Mismatches 7; Indels 2; Gaps 1;

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Seq. No. 17;
Mismatches 7; Indels 2; Gaps 1;

DB 49; DB 2; Local: 1000;
Seq. No. 17;
Mismatches 7; Indels 2; Gaps 1;

DB 49; DB 2; Local: 1000;
Seq. No. 17;
Mismatches 7; Indels 2; Gaps 1;



Version 5.1.3
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W-1000 / Search time: 10.0 seconds
/without alignment
117,278 Malignant cell updates/sec

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W-1000

W-1000

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35 43 41.3 422 1 KAS1_STBHA
36 43 41.3 424 1 CP3_MOUSE
37 43 41.3 425 1 YIF1_FEAST
38 43 41.3 705 1 ADDG_FAT
39 43 41.3 706 1 ADDG_HUMAN
40 43 41.3 706 1 ADDG_MOUSE
41 43 41.3 913 1 PKF5_HUMAN
42 43 41.3 914 1 PKF5_MOUSE
43 43 41.3 1877 1 PKF5_MOUSE
44 43 41.3 1877 1 PKF5_MOUSE
45 43 41.3 2492 1 ATRX_HUMAN

ALIGNMENTS

RESULT 1
MACS_BOVIN STANDARD; PRT; 331 AA.
AC P12624;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Myristoylated alanine-rich C-kinase substrate (MARCKS)
GN MARCKS CP MACS
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovina; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID:9913;
RN [1]
RP MEDLINE:9992412; PubMed:2734117;
RA Stumpo D J, Graff J M, Albert K A, Greenstadt P, Blackshear P L;
PT "Nucleotide sequence of a cDNA for the bovine myristoylated
alanine-rich C-kinase substrate (MARCKS).";
RL Nucleic Acids Res. 17:3887-3988(1989).
RN [2]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
PX MEDLINE:9992453; PubMed:2727623;
RA Stumpo D J, Graff J M, Albert K A, Greenstadt P, Blackshear P L;
PT "Molecular cloning, characterization, and expression of a cDNA
encoding the 180 to 270 aa myristoylated alanine-rich C-kinase
substrate: a major cellular substrate for protein kinase C.";
PL Proc Natl Acad Sci USA 87:4015-4018(1990).
RN [3]
RP PARTIAL SEQUENCE.
PX MEDLINE:9217108; PubMed:1540183;
RA Mizutani A, Tokumitsu H, Hidaka H;
PT "Acidic calmodulin binding protein, ACAP-81, is MARCKS protein
interacting with synapsin I.";
PL Biochem Biophys Res Commun. 192:1195-1401(1992).
RN [4]
RP PHOSPHORYLATION SITES.
PX MEDLINE:9308594; PubMed:2473066;
RA Graff J M, Stumpo D J, Blackshear P J;
PT "Characterization of the phosphorylation sites in the chicken and
bovine myristoylated alanine-rich C-kinase substrate protein. A
prominent cellular substrate for protein kinase C.";
PL J Biol Chem 264:11912-11919(1989).
RN [5]
RP PHOSPHORYLATION SITES, AND DEVIATIONS.
PX MEDLINE:9410952; PubMed:9034575;
RA Taniguchi H, Marenzi S, Suzuki M, Titani K;
PT "Myristoylated alanine-rich C-kinase substrate (MARCKS), a major
protein kinase C substrate, is an in vivo substrate of
protein kinase C. A mass spectrometric analysis of
the post-translational modifications.";
PL J Biol Chem 269:19200-19206(1994).
RN [6]
RP REVERSIBLE ASSOCIATION WITH THE MEMBRANE.

EF Glycylglycyl-N-terraninyltransferase 1 (P01410) (Peptidyl-N
DE myristoyltransferase 1) (Myristoyl-CoA-protein N-myristoyltransferase
DE 1) (NMT 1) (Type I N-myristoyltransferase).
GN NMT1 OR NMT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Mammalia; Primates; Homi-
OC Mammalia; Eutheria; Primates; Catarrhini; Homi-
ON NCBI_TaxID:9606;
RX MEDLINE:9606;
RP SEQUENCE OF 55 496 FROM N.A. AND MUTAGENESIS OF 496
RX MEDLINE:9606;
PA Duronio P.J., Reed S.L., Gordon J.I.;
PT "Mutations of human myristoyl-CoA-protein N-myristoyltransferase
PT cause temperature-sensitive myristic acid deficiency in Saccharomyces
PT cerevisiae".
RL Proc. Natl. Acad. Sci. U.S.A. 89:4129-4133(1992).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE:9606;
RA Glover C.J., Hartman K.D., Pelster P.L.;
PT "Human N-myristoyltransferase amino terminal domain involved in
PT targeting the enzyme to the ribosomal subcellular fraction".
RL J. Biol. Chem. 272:28690-28694(1997).
RN [3]
RN SEQUENCE FROM N.A.
RC TISSUE-Brain;
RX MEDLINE:98175914; PubMed 9506952;
RA Giang D.K., Clavette B.F.;
PT "A second mammalian N-myristoyltransferase".
RL J. Biol. Chem. 272:12595-12599.
RN [4]
RN SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
RC TISSUE-Muscle, and SKIN;
RA Strausberg R.;
RL Submitted (MAY-2000) to the EMBL/GenBank/Tran databases
RN [5]
RN SEQUENCE OF 81 89 FROM N.A.
RX MEDLINE:98143033; PubMed 9677104.
RA Mathiasen K.A., Young K., Egelon M., Carlie R., White A.,
RA Skolovick M.;
PT "Characterization of human and rat brain myristoyl-CoA protein
PT N-myristoyltransferase: evidence for an alternative splicing variant of
PT the enzyme".
RL Biochem. J. 331:421-425(1998).
CC [1]
CC FUNCTION: Adds a myristoyl group to the N terminal glycine residue
CC of certain cellular and viral proteins.
CC [2]
CC CATALYTIC ACTIVITY: tetradecanoyl-CoA + glycyl peptide = CoA + N-
CC tetradecanoylglycyl-peptide.
CC [3]
CC SUBCELLULAR LOCATION: Cytoplasmic.
CC [4]
CC ALTERNATIVE INTRON 2 EXONS; a long form (shown here) and a
CC short form, are produced by alternative splicing.
CC [5]
CC TISSUE SPECIFICITY: HEART, GUT, KIDNEY, LIVER, AND PLACENTA
CC [6]
CC SIMILARITY: BELONGS TO THE NMT FAMILY.

CC This SWISS-PROT entry is a duplicate. It is identical with a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by any third party. Institutions as long as they agree in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement. See http://www.ebi.ac.uk/arc4/arc4-
CC or send an email to license@ebi.ac.uk.

CC EMBL: M86701; JCT ANNOTATED CDS.
CC EMBL: AF041324; AAC05294.1; ALT_INIT
CC EMBL: AF020500; AAB96316.1;
CC EMBL: BC006538; AAB06538.1;
CC EMBL: BC006549; AAB06549.1;
CC EMBL: BC007259; AAB07259.1;
CC EMBL: BC008412; AAB08412.1;
CC EMBL: Y17225; CAA76686.1;
CC PIR: JCI143; JCI143.
CC HSP: P30418; NMT.
CC GenBank: U0957; NMT1.

TF MM, 152993;
TF Invertebrata; Insecta; Nmt.
TF Pfam: PF02799; NMT_1;
TF Pfam: PF02799; NMT_C1;
TF PROSITE: PS00975; NMT_1;
TF PROSITE: PS00975; NMT_C1;
TF TRANSFERASE: Acyltransferase; Alternative splicing.
TF DOMAIN 55 47 POLY-LYS (IN SHORT ISOFORM).
TF VARSPLIC 1 80 MISSING (IN SHORT ISOFORM).
TF MUTAGEN 496 492 MISSING (IN SHORT ISOFORM).
TF MUTAGEN 496 492 MISSING (IN SHORT ISOFORM).
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CC Matched 46 98; Pos 1; Length 496;
CC 1 SPSENETPPPPPPPPPPPP 18
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CC NMT1_MOUSE
CC ID NMT1_MOUSE STANDARD; PRT; 496 AA.
CC AC 070310;
CC DT 30-MAY-2000 (Ref. 39, Created)
CC DT 30-MAY-2000 (Ref. 39, Last sequence update)
CC DT 15-JUN-2002 (Ref. 41, Last annotation update)
CC DE Glycylglycyl-N-terraninyltransferase 1 (P01410) (Peptidyl-N-
CC tetradecanoyltransferase 1) (Myristoyl-CoA-protein N-myristoyltransferase
CC 1) (NMT 1) (Type I N-myristoyltransferase).
CC GN NMT1
CC OS Mus musculus (Mouse)
CC OC Eukaryota; Metazoa; Chordata; Mammalia; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC OX NCBI_TaxID=10090;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC TISSUE-Liver;
CC EX MEDLINE:98175914; PubMed 9506952;
CC RA Giang D.K., Clavette B.F.;
CC PT "A second mammalian N-myristoyltransferase".
CC RL J. Biol. Chem. 272:12595-12599(1998).
CC RN [2]
CC RP SEQUENCE FROM N.A.
CC RA Strausberg R.;
CC BL Submitted (MAY-2000) to the EMBL/GenBank/Tran databases
CC CC [3]
CC CC FUNCTION: Adds a myristoyl group to the N terminal glycine residue
CC of certain cellular and viral proteins.
CC [4]
CC CATALYTIC ACTIVITY: tetradecanoyl-CoA + glycyl peptide = CoA + N-
CC tetradecanoylglycyl-peptide.
CC [5]
CC ALTERNATIVE INTRON 2 EXONS; a long form (shown here) and a
CC short form, are produced by alternative splicing.
CC [6]
CC TISSUE SPECIFICITY: HEART, GUT, KIDNEY, LIVER, AND PLACENTA
CC [7]
CC SIMILARITY: BELONGS TO THE NMT FAMILY.

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CC use by any third party. Institutions as long as they agree in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement. See http://www.ebi.ac.uk/arc4/arc4-
CC or send an email to license@ebi.ac.uk.

CC EMBL: M86701; JCT ANNOTATED CDS.
CC EMBL: AF041324; AAC05294.1; ALT_INIT
CC EMBL: AF020500; AAB96316.1;
CC EMBL: BC006538; AAB06538.1;
CC EMBL: BC006549; AAB06549.1;
CC EMBL: BC007259; AAB07259.1;
CC EMBL: BC008412; AAB08412.1;
CC EMBL: Y17225; CAA76686.1;
CC PIR: JCI143; JCI143.
CC HSP: P30418; NMT.
CC GenBank: U0957; NMT1.

61FA78854A50F3B0 (P. 4)

Score 48; DB 1; Length 497

Best Local Similarity 55.6%; Pred. No. 9.2;

Mismatches 5; Indels 0; Gaps 0;

Query Match 46.2%; Score 48; DB 1; Length 497;

Best Local Similarity 55.6%; Pred. No. 9.2;

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Best Local Similarity 55.6%; Pred. No. 9.2;

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Mismatches 5; Indels 0; Gaps 0;

as as long as it remains in no way
not removed. Usability and for commercial
content (See <http://www.intel.nl/ch/announce/>
; site.ch).

hydroxylation; Enzyme purification.
 © SEPHYLATION BY PPA BY SIMILARITY.
 5, 5 IN PG.
 "FA099E2HVD0216 2004"

version 5.1.3
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Standard Error

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suits predicted by class 1 have a score of the model being printed, the total score distribution.

Summary

Classification

- Kingdom Animalia
- Phylum Chordata
- Class Mammalia
- Order Artiodactyla
- Suborder Ruminantia
- Superfamily Bovidae
- Family Bovidae
- Genus Bos
- Species Bos taurus

17	47	45.2	170	5	Q44172	CaM172	CaM172
18	47	45.2	863	10	Q9LEER	Q9LEER	Q9LEER
19	47	45.2	1714	5	Q9L22C	Q9L22C	Q9L22C
20	47	45.2	2029	5	Q9V0V7	Q9V0V7	Q9V0V7
21	46	44.2	85	12	Q55718	Q55718	Q55718
22	46	44.2	351	4	Q9VU21	Q9VU21	Q9VU21
23	46	44.2	351	5	Q21635	Q21635	Q21635
24	46	44.2	358	11	Q9QZ09	Q9QZ09	Q9QZ09
25	46	44.2	418	11	Q9ER10	Q9ER10	Q9ER10
26	46	44.2	600	5	Q9VNG1	Q9VNG1	Q9VNG1
27	46	44.2	661	11	Q9ROV4	Q9ROV4	Q9ROV4
28	46	44.2	703	5	Q960X1	Q960X1	Q960X1
29	46	44.2	375	5	Q9W731	Q9W731	Q9W731
30	46	44.2	930	11	Q9QBM1	Q9QBM1	Q9QBM1
31	46	44.2	930	5	Q9V0E5	Q9V0E5	Q9V0E5
32	46	44.2	1004	5	Q9E167	Q9E167	Q9E167
33	45.5	43.8	685	5	Q81253	Q81253	Q81253
34	45.5	43.8	667	5	Q9VMY3	Q9VMY3	Q9VMY3
35	45.5	43.8	1445	3	Q04291	Q04291	Q04291
36	45	43.3	115	11	Q9D9P0	Q9D9P0	Q9D9P0
37	45	43.3	245	6	Q9PSE3	Q9PSE3	Q9PSE3
38	45	43.3	268	10	Q9PHC2	Q9PHC2	Q9PHC2
39	45	43.3	294	12	Q91S33	Q91S33	Q91S33
40	45	43.3	294	12	Q91B40	Q91B40	Q91B40
41	45	43.3	294	12	Q91P39	Q91P39	Q91P39
42	45	43.3	294	12	Q91R38	Q91R38	Q91R38
43	45	43.3	294	12	Q91P27	Q91P27	Q91P27
44	45	43.3	294	12	Q91R35	Q91R35	Q91R35
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ALIGNMENTS

RESULT 1

094503	Genes	PREDIMINARY:	REF: 247 AA
ID	093503;		
AC	093503;		
DT	01-NOV-1998 (Tremburel 08, Created:		
DT	01-NOV-1998 (Tremburel 08, Last sequence up		
DT	01-DSC-2001 (Tremburel 12, Last annotation		
DE	Myristoylated alanine-rich C kinase substrat		
GN	MARCKS.		
OS	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Verte		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; P		
OC	Xenopodinae; Xenopus.		
OX	NCBI_TaxID=8355;		
RN	[1]		
PP	SEQUENCE FROM N.A.		
RX	MEDLINE=36030614; PubMed=9361009;		
RA	Shi Y., Sullivan S.K., Pitterle D.M., Kennin		
RA	Blackshear P.J.		
RT	"Mechanisms of MARCKS gene activation during		
RL	J. Biol. Chem. 273:29226-29230(1997).		
DR	EMBL; AF017299; AAC61897.1; ..		
DR	InterPro; IP002101; MARCKS.		
DR	RefSeq; PF02044; MAPKRS; 1.		
DR	PRINTS; PS00963; MARCKS.		
DR	PROSITE; PS00826; MARCKS 1; 1-		
DR	PROSITE; PS00827; MARCKS_2; 1.		
KW	Kinase.		
SQ	SEQUENCE 297 AA; 1914; MW: 35CB/ABREVISED		

Cover Material	96 58	Servo 30	ED 13
Resistor Smelliness	94 78	FWD NO.	96-06
Matches	18	Conservative	1 Index
Qv	1	Servos	19
ED	11B	Servos	16

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Best Local Similarity	94.78;	Pred. NO.	9e-06;	

Best local similarity	94.78	Pred. No. 9e-35;
Matches	18	Conservative
		0; Mismatches
		1; Indels
		0; Gaps

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Q87850
ID Q87850 PRELIMINARY; PRT; 286 AA.
AC C8Y850;
DT DT 01-MAR-2002 (TrEMBLrel_19, Created).
DT DT 01-MAR-2002 (TrEMBLrel_20, Last sequence update).
DE DE 01-MAR-2002 (TrEMBLrel_20, Last annotation update).
DE Hypothetical protein IM0068.
GN IM0068.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Listeriaceae; Listeria.
NCBI TaxID=1639;
(1) _TaxID=1639;
SEQUENCE FROM N.A.
RP STRAIN:EHEC / SERVAP 120A;
RX MEDLINE=2153279, PubMed=11679669;
RA Glauber P., Frangeul L., Buchrieser C., Rusnick C., Arnaud A.,
RA Baquero F., Berche P., Blocher H., Bianci P., Chararabery T.,
RA Charrat A., Cherouani F., Couve E., de Lariva A., Debovy I.,
RA Domann K., Dominguez-Bernal G., Duchaud E., Dutari L., Escudérot G.,
RA Gautier L., Goebel W., Gomez-Izquierdo N., Hain T., Haut J., Jackson R.,
RA Jones I.-M., Karst U., Kreft J., Kuhn M., Kuster F., Kurakpa G.,
RA Madueno E., Mailhotnam A., Mata Vicente J., Ng E., Nedjati A.,
RA Nordisk G., Novella S., de Pablo B., Perez-Diaz J.-C., Putelli F.,
RA Remmel B., Rose M., Schlatter T., Simoes N., Tiertez A.,
RA Vazquez-Rolland J.-A., Vois H., Weiland J., Zornot P.;
PT "Comparative genomics of Listeria species.";
RRL Scienc 204:40-45(2001);
DR EMU; AF591977; CAG99146.1; -.
DL Listlist; LM001068; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 286 AA; 3078 MW; F1DCC5B1AACA 1P44;

Query Match 46.3%; Score 48; DB 16; Length 286;
Best Local Similarity 50.63; Pval No. 18;
Matches 11; Conservative 2; Mismatches 7; Indels 0; Gaps
CY 1 SPSENPZY...KYZPPFPFZSG 20
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DB 87 TPETTRSPATTEAFSSISG 109

RESULT 15
Q96H14 PRELIMINARY; PRT; 478 AA.
ID Q96H14;
AC Q96H14;
DT DT 01-DEC-2001 (TrEMBLrel_19, Created).
DT DT 01-DEC-2001 (TrEMBLrel_19, Last sequence update).
DE DE 01-MAR-2002 (TrEMBLrel_20, Last annotation update).
DE Similar to N-myristoyltransferase 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
NCBI TaxID=9606;
(1) _TaxID=9606;
SEQUENCE FROM N.A.
RP TISSUE=BRAIN;
RC Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
RF EMBL; BC008579; AAH08579.1; -.
DR InterPro; IPRO00903; Nmt.
DR Pfam; PF01233; NMT_1.
DR Pfam; PF02799; NMT_C_1.
DR PROSITE; PS00975; NMT_1; UNKNOWN_1.
DR PROSITE; PS00976; NMT_2; UNKNOWN_1.
DR Transferrase.
RW SEQUENCE 478 AA; 54944 MW; tAD9CAZELBLSQLD CP6644;

Query Match 46.3%; Score 48; DB 4; Length 478;

```

QY 1 SPONETPPPPPPPPPP 18
DT 00 SPONETPPPPPPPPPP 45

Search completed: March 3, 2003, 06:14:49
Job time : 46.4146 secs


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RESULT 4
US-09-999-745-42
? Sequence 42, Application US/09554000
? Patent No. US2002015720A1
? GENERAL INFORMATION:
? APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
? APPLICANT: Tsien, Roger Y.
? APPLICANT: Baird, Geoffrey
? TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
? FILE REFERENCE: REGEN1470-1
? CURRENT APPLICATION NUMBER: US/09/999,745
? PRIOR FILING DATE: 1999-03-14
? PRIOR APPLICATION NUMBER: US/99/042,001
? NUMBER OF SEQ ID NOS: 21
? SOFTWARE: Patent in version 3.0
? SEQ ID NO 42
? LENGTH: 25
? TYPE: PRT
? ORGANISM: Rattus norvegicus
US-09-999-745-42

Query Match: 57.9%, Score: 60, DB: 9, Length: 25,
Best Local Similarity: 100%, Prod No: 6,
Matches: 12; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 9 KKKKKPSPEK 19
DB 1 KKKKKPSPEK 12

RESULT 5
US-09-554-000-27
? Sequence 27, Application US/09554000
? Patent No. US2002015720A1
? GENERAL INFORMATION:
? APPLICANT: Tsien, Roger Y.
? APPLICANT: Miyawaki, Atsushi
? TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
? TITLE OF INVENTION: DETECTION OF ANALYTES
? FILE REFERENCE: 02357/042001
? CURRENT APPLICATION NUMBER: US/09/554,000
? PRIOR FILING DATE: 1999-03-14
? PRIOR APPLICATION NUMBER: 02357/042001
? NUMBER OF SEQ ID NOS: 56
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 27
? LENGTH: 24
? TYPE: PRT
? ORGANISM: Mus musculus
US-09-554-000-27

Query Match: 49.1%, Score: 42, DB: 9, Length: 24,
Best Local Similarity: 100%, Prod No: 1,
Matches: 9; Conservative: 1; Mismatches: 0; Indels: 0; Gaps: 0;

QY 9 KKKKKPSPEK 18
DB 1 KKKKKPSPEK 10

RESULT 6
US-09-884-681-8
? Sequence 8, Application US/09554000
? Patent No. US2002015720A1
? GENERAL INFORMATION:
? APPLICANT: Tsien, Roger Y.
? APPLICANT: Cubitt, Andrew B.
? TITLE OF INVENTION: Assays for Protein Kinases Using
? TITLE OF INVENTION: Fluorescent Protein Substrates
? NUMBER OF SEQUENCES: 48
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Townsend and Townsend and Crew LLP
? STREET: Two Embarcadero Center, Eighth Floor
? CITY: San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 94111-3834
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible

```

```

? FILE REFERENCE: REGEN1470-1
? CURRENT APPLICATION NUMBER: US/09/999,745
? PRIOR FILING DATE: 1999-03-14
? PRIOR APPLICATION NUMBER: US/99/042,001
? NUMBER OF SEQ ID NOS: 21
? SOFTWARE: Patent in version 3.0
? SEQ ID NO 43
? LENGTH: 24
? TYPE: PRT
? ORGANISM: Mus musculus
US-09-999-745-43

Query Match: 49.2%, Score: 48, DB: 9, Length: 24,
Best Local Similarity: 100%, Prod No: 1,
Matches: 9; Conservative: 1; Mismatches: 0; Indels: 0; Gaps: 0;

QY 9 KKKKKPSPEK 18
DB 1 KKKKKPSPEK 10

RESULT 5
US-09-554-000-27
? Sequence 27, Application US/09554000
? Patent No. US2002015720A1
? GENERAL INFORMATION:
? APPLICANT: Tsien, Roger Y.
? APPLICANT: Miyawaki, Atsushi
? TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
? TITLE OF INVENTION: DETECTION OF ANALYTES
? FILE REFERENCE: 02357/042001
? CURRENT APPLICATION NUMBER: US/09/554,000
? PRIOR FILING DATE: 1999-03-14
? PRIOR APPLICATION NUMBER: 02357/042001
? NUMBER OF SEQ ID NOS: 56
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 27
? LENGTH: 24
? TYPE: PRT
? ORGANISM: Mus musculus
US-09-554-000-27

Query Match: 49.1%, Score: 42, DB: 9, Length: 24,
Best Local Similarity: 100%, Prod No: 1,
Matches: 9; Conservative: 1; Mismatches: 0; Indels: 0; Gaps: 0;

QY 9 KKKKKPSPEK 18
DB 1 KKKKKPSPEK 10

RESULT 6
US-09-884-681-8
? Sequence 8, Application US/09554000
? Patent No. US2002015720A1
? GENERAL INFORMATION:
? APPLICANT: Tsien, Roger Y.
? APPLICANT: Cubitt, Andrew B.
? TITLE OF INVENTION: Assays for Protein Kinases Using
? TITLE OF INVENTION: Fluorescent Protein Substrates
? NUMBER OF SEQUENCES: 48
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Townsend and Townsend and Crew LLP
? STREET: Two Embarcadero Center, Eighth Floor
? CITY: San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 94111-3834
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible

```



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US-10-003-671A-23
; Sequence 23, Application US/10000671A
; Patent No. US600015600A1
; GENERAL INFORMATION:
; APPLICANT: MIZE, ET AL
; TITLE OF INVENTION: NOVEL INTERLEUKIN-1 HVC MATERIALS AND METHODS
; CURRENT APPLICATION NUMBER: US/10/003,671A
; FILE REFERENCE: 08110/36859A
; PRIORITY FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 00/245,346
; PRIOR FILING DATE: 2000-11-02
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 23
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-003-671A-23

Query Match 42.3%; Score 44, DP 0, Length 151,
Best Local Similarity 52.9%; Pred. No. 34;
Matches 9, Conservative 1, Mismatches 7, Indels 0, Gaps 0,

Cy 2 FNNETRYKKYKFFSPKK 18
Db 95 PNYVYKZYKZYKFFVYK 101

RESULT 10
US-10-095-407-15
; Sequence 15, Application US/1000407
; Patent No. US2002014330A1
; GENERAL INFORMATION:
; APPLICANT: ERI, YAKU
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO 77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/10/004,407
; PRIORITY FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 00/034,640
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: US 00/054,640
; PRIOR FILING DATE: 1997-09-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FASTA32 for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-095-407-15

Query Match 42.3%; Score 44, DP 0, Length 153,
Best Local Similarity 52.9%; Pred. No. 34,
Matches 9, Conservative 1, Mismatches 7, Indels 0, Gaps 0,

Cy 2 FNNETRYKKYKFFSPKK 18
Db 97 PNYVYKZYKZYKFFVYK 103

RESULT 11
US-10-139-833-8
; Sequence 8, Application US/10139833
; Publication No. US20030004106A1
; GENERAL INFORMATION:
; APPLICANT: Garis, Christian M.
; APPLICANT: Giles, Jennifer
; APPLICANT: Mu, Sharon X.
; APPLICANT: Xia, Min
; APPLICANT: Bass, Michael B.
; APPLICANT: Cravetto, Roger
; TITLE OF INVENTION: A Novel Interleukin-1 Receptor Antagonist-Related Molecules and
; TITLE OF INVENTION Uses Thereof

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; FILE REFERENCE: 00-1213-E
; CURRENT APPLICATION NUMBER: US/10/130,833
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/170,191
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/182,063
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: 60/194,521
; PRIOR FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 60/195,910
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: 02/724,583
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent in Ver. 3.0
; SEQ ID NO 8
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-130-833-8

Query Match 42.3%; Score 44, DP 0, Length 153,
Best Local Similarity 52.9%; Pred. No. 34;
Matches 9, Conservative 1, Mismatches 7, Indels 0, Gaps 0,

Cy 2 FNNETRYKKYKFFSPKK 18
Db 87 PNYVYKZYKZYKFFVYK 103

RESULT 12
US-09-775-046-6
; Sequence 6, Application US/0975046
; Patent No. US2000010234A1
; GENERAL INFORMATION:
; APPLICANT: Deters, Johannes Edward Maria Antonius
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Pazan, J. Fernando
; APPLICANT: Kastlein, Robert A.
; TITLE OF INVENTION: MAMMALIAN TGF-BETAS, RELATED PEPTIDES AND METHODS
; FILE REFERENCE: 0201073X
; CURRENT APPLICATION NUMBER: US/09/775,046
; CURRENT FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/179,638
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 6
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-775-046-6

Query Match 42.3%; Score 41, DP 10, Length 153,
Best Local Similarity 52.9%; Pred. No. 34;
Matches 9, Conservative 1, Mismatches 7, Indels 0, Gaps 0,

Cy 2 FNNETRYKKYKFFSPKK 18
Db 97 PNYVYKZYKZYKFFVYK 103

RESULT 13
US-09-770-528-10
; Sequence 10, Application US/09770528
; Patent No. US20020164332A1
; GENERAL INFORMATION:
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Sara, Theodore P.
; APPLICANT: Bazan, Fernando J.
; APPLICANT: Kastlein, Robert A.
; TITLE OF INVENTION: Mammalian Cy Kinase Related Reagents
; TITLE OF INVENTION and Methods

```


CC Invention relates to methods of inhibiting mucus secretion by a
 CC mucus secreting cell by administering a compound that inhibits
 CC MAPKs protein-related mucus secretion. Such compounds include
 CC active fragments of MAPKs protein such as MAPK peptide (see
 CC AAY95997) and MA-PKS peptide (see AAY95997), which corresponds to a
 CC phosphorylation site of MAPKs. The inhibitory compounds can be
 CC used to treat conditions such as bronchitis, cystic fibrosis,
 CC chronic obstructive pulmonary disease, asthma, emphysema,
 CC pneumonia, influenza, rhinitis and the common cold. An alternative
 CC sequence for MAPKs is provided in AAY95999, which differs from the
 CC present sequence at 2 amino acid residues, Ala 84 (Ser) and
 CC Pro-119 (Ala).

XX Sequence 332 AA;

Query Match 94.23, Score 98, EP 01, Length 332;
 Best Local Similarity 100.00, Prod No. 1.7e-06;
 Matches 19, Conservative 0, Mismatches 0, Indels 0, Gaps 0.

QY 1 SPSTNETPPPPPPPPPPPPPPPS 19
 ||||| ||||| ||||| ||||| |||||

DB 145 SPSTNETPPPPPPPPPPPPPPPS 163

RESULT 6

AAV95999
 ID AAY95999 standard; Protein; 332 AA.

XX AAY95999;

DT 20-NOV-2000 (first entry)

DE Human myristoylated alanine rich C kinase substrate MAPKs.

FW MAPKs; myristoylated alanine-rich C kinase substrate; human;
 FW mucus secreting, inhibitory; bronchitis, asthma, cystic fibrosis,
 FW chronic obstructive pulmonary disease; pneumonia; emphysema;
 FW influenza, rhinitis, therapy.

OS Homo sapiens

XX Key Location/Qualifiers

FT Misc-difference 94 /note= "Ala in sequence of AAY95999"

FT Misc-difference 119 /note= "Pro in sequence of AAY95999"

FT Peptide 2...25 "MA-PKS peptide of AAY95999"

FT Peptide 152..176

FT /note= "MA-PKS peptide of AAY95999"

XX W0900590002 A2.

PN 31-AUG-2000.

PD 24 FEB 2000, 2000W0-0000-0000

PF 24 FEB 1999, 2000 0256154.

PR (UNIV) UNIV NORTH CAROLINA STATE.

XX Li Y, Martin LD, Adler KB;

DR WPI; 2000 572036/53

DP N-PSDB; AAY95999.

XX Regulating mucus secretion by a mucus-secreting cell, useful for
 PT treating e.g. bronchitis, asthma or pneumonia, by administering a
 PT compound that inhibits or enhances myristoylated alanine rich C kinase
 PT substrate protein.

XX Disclosure; Page 46-47; 56pp; English.

CC The present sequence is that of human myristoylated alanine rich C
 CC kinase substrate MAPKs protein, a major cellular substrate. The
 CC invention relates to methods of inhibiting mucus secretion by a
 CC mucus-secreting cell by administering a compound that inhibits
 CC MAPKs protein-related mucus secretion. Such compounds include
 CC active fragments of MAPKs protein such as MAPK peptide (see
 CC AAY95997) and MA-PKS peptide (see AAY95997), which corresponds to a
 CC phosphorylation site of MAPKs. The inhibitory compounds can be
 CC used to treat conditions such as bronchitis, cystic fibrosis,
 CC chronic obstructive pulmonary disease, asthma, emphysema,
 CC pneumonia, influenza, rhinitis and the common cold. An alternative
 CC sequence for MAPKs is provided in AAY95999, which differs from the
 CC present sequence at 2 amino acid residues, Ser-84 (Ala) and
 CC Ala-119 (Pro).

XX Sequence 332 AA;

Query Match 94.23, Score 98, EP 01, Length 332;
 Best Local Similarity 100.00, Prod No. 1.7e-06;
 Matches 19, Conservative 0, Mismatches 0, Indels 0, Gaps 0.

QY 1 SPSTNETPPPPPPPPPPPPPPPS 19
 ||||| ||||| ||||| ||||| |||||

DB 145 SPSTNETPPPPPPPPPPPPPPPS 163

RESULT 7

AAV95999
 ID AAY95999 standard; Protein; 330 AA.

XX AAY95999;

DT 23-OCT-1990 (first entry)

DE High density lipoprotein (HDL) binding protein.

FW High density lipoprotein (HDL) binding protein; hypercholesterolemia;
 FW hypercholesterolaemia; ds.

OS Homo sapiens

XX W09005744-A.

XX 31-MAY-1990.

XX 17-NOV-1989, 89W0-0000169.

XX 18 NOV 1989, 89US 0273388.

XX (UNIV) UNIV OF WASHINGTON.

XX (UNIV) ZYMOGENETICS INC.

PI Oram JF, McKnight GL, Hart CE, Curtis DA;

XX WPI; 1990-193405/25.

XX N-PSDB; AAY95999.

XX New mammalian proteins binding high density lipoprotein sub-class 3
 PT DNA encoding them and derived antibodies, for screening
 PT potentially therapeutic HDL analogues and for diagnosing risk of
 PT atherosclerosis.

XX Claim 4; Fig 1A-D; 79pp; English.

XX The protein product may be used to raise Abs, and the cDNA to
 CC create probes, both useful in screening for HDL analogues,
 CC agonists and antagonists, and in identifying abnormalities in the
 CC HDL binding/secretion pathway. HDL analogues can be used in treating
 CC hypercholesterolemia and atherosclerosis.

XX Sequence 330 AA;

Query Match 62.5%; Score 65; DB 11; Length 330;

Mismatches 0; Gaps 0;

AA

21-JUN-2000 (first entry)

XX

Anticardiac, antithrombotic, affinity filter, anionic phospholipid,

XX

cell surface; binding agent; procoagulant macrophages; apoptosis; cell

XX

cell debris; F-4; extracellular matrix; platelets; thrombosis;

XX

plasmapheresis, surgery, hemodialysis, diabetes, thalassemia;

XX

systemic lupus erythematosus; thrombocytopenia;

XX

Synthetic.

OS

Key

XX

Location/Qualifiers

PH

Modified-site 1

FT

/note= "conjugated to myristate group"

FT

Modified-site 26

FT

/note= "conjugated to biotin, an anchoring moiety of a

FT

moiety comprising a 'unsaturated fatty acid

FT

acid polyunsaturated < 200 fatty acid, a cyclo

FT

residue bound to a 5-10C prenyl group through

FT

a thioether bond, where the moiety is linked

FT

through an amide bond"

FT

WO200010673-A1.

PN

02-MAR-2000.

XX

23-AUG-1999; 99WO-1100459.

XX

24-AUG-1998; 98IL-0125908.

XX

27-NOV-1998; 98US-0200715.

PR

05-AUG-1999; 99IL-0131266.

PR

(NSTN) NST NEUROCURVIVAL TECHNOLOGIES LTD.

XX

Ziv I, Shirvan A;

XX

WPI; 2000-25549/22.

XX

Affinity filter for treating biological fluids, used e.g. to remove

XX

prothrombotic particles from blood and for detecting apoptosis.

XX

Contains agent that binds specifically to anionic phospholipid exposed

XX

on cell surface .

XX

Claim 27, 28; Page 48, 49; 95pp; English.

PS

The invention relates to novel affinity filter (AF) for capturing or

XX

removing particles having exposed anionic phospholipids on the surface,

XX

from a biological fluid comprises a body containing a solid support that

XX

has, linked to it, a binding agent that is specific for exposed anionic

XX

phospholipid. The binding agents are especially fatty acids such as

XX

phospholipids having a hydrophobic moiety and a hydrophilic moiety,

XX

Query Match 57.7%; Score 60; DB 21; Length 24;

Best Local Similarity 100.0%; Pred. No. 0.051;

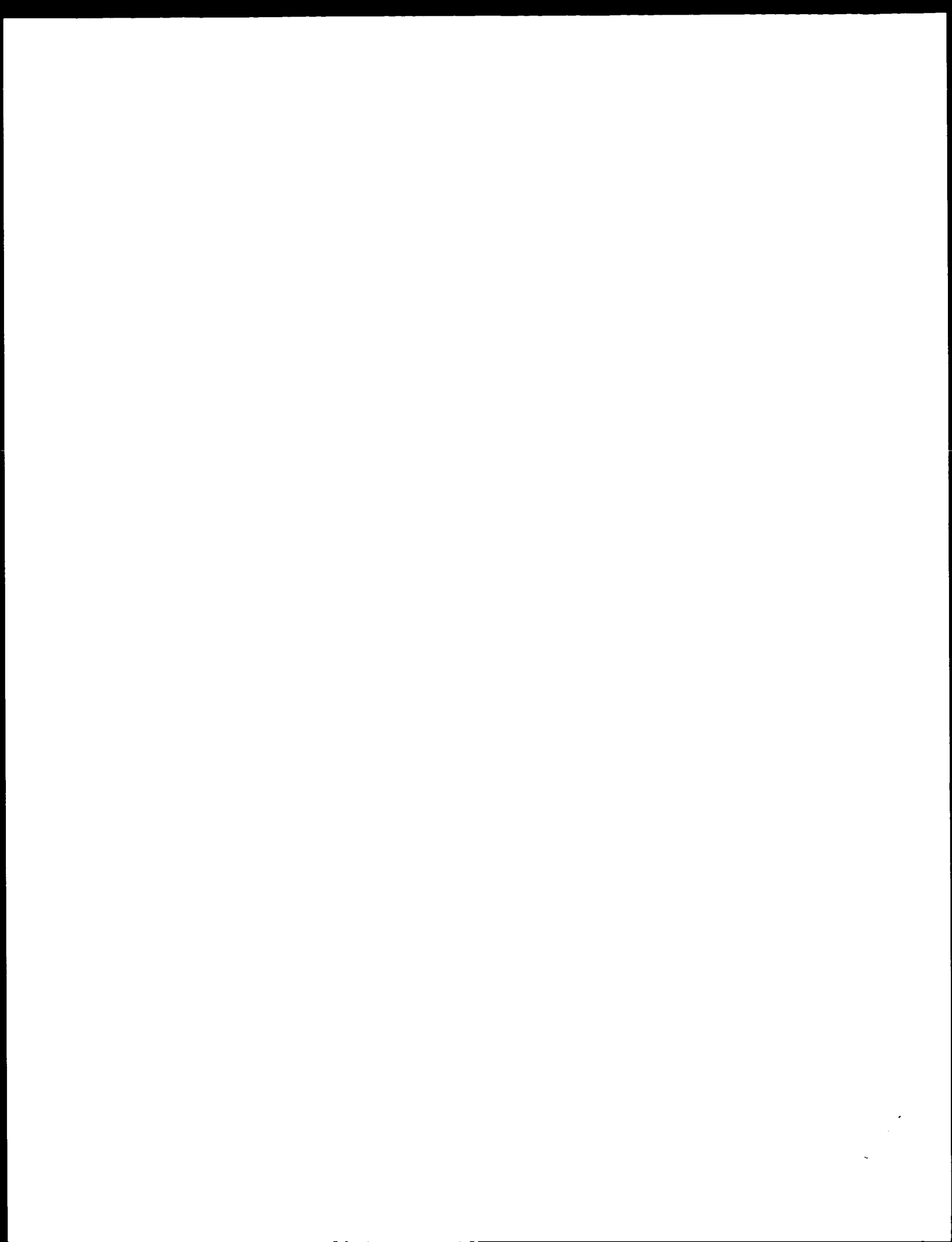
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

9 KKKKKPSPKKS 19

|||||

Sequence 26 AA;

AA



11	65	78.3	17	23	ABB1235	Anti-thrombin, rept
12	58	69.9	20	21	ABE26819	Peptide membrane
13	55	66.3	182	22	AAO3872	Human polypeptide
14	53	63.9	157	22	AAO6556	Human polypeptide
15	52	62.7	119	22	AAO18164	N-terminus of human
16	51	61.4	40	22	AAO33146	Human polypeptide
17	51	61.4	90	21	AAO3790	Human polypeptide
18	51	61.4	117	22	AAO7791	Human polypeptide
19	51	61.4	133	22	AAO10133	Human polypeptide
20	51	61.4	702	22	AAE35147	Human SPAN-1, SEC 1
21	51	61.4	764	22	ABE22230	Novel human diatom
22	51	61.4	894	22	AAE35148	Human NFAP-1, SEC 1
23	51	61.4	946	22	ABE22233	Novel human diatom
24	50	60.2	209	21	AAV95630	Human parathyroid
25	49	59.0	59	22	AAE35897	Human parathyroid
26	49	59.0	79	11	AAE96980	PTHrP, 1-34, peptide
27	49	59.0	101	22	ABE35643	Peptide #2048, eno
28	49	59.0	101	22	ABE24274	Protein #2273, eno
29	49	59.0	101	22	AAE35641	Human PTHrP, eno
30	49	59.0	101	22	AAE35645	Human PTHrP, eno
31	49	59.0	101	22	AAE35647	Peptide #1194, eno
32	49	59.0	101	23	ABE35648	Human PTHrP, eno
33	49	59.0	133	23	AAE23744	Human PTHrP, eno
34	49	59.0	135	23	AAE23745	Human PTHrP, eno
35	49	59.0	139	23	AAE23750	Human PTHrP, eno
36	49	59.0	139	23	AAO14630	Human PTHrP, eno
37	49	59.0	139	23	ABE04991	Human PTHrP, eno
38	49	59.0	141	17	AAE99452	Human PTHrP, eno
39	49	59.0	141	23	AAE23749	Human PTHrP, eno
40	49	59.0	141	23	AAO14631	Human PTHrP, eno
41	49	59.0	141	23	ABE04992	Human PTHrP, eno
42	49	59.0	173	23	AAO14632	Human PTHrP, eno
43	49	59.0	173	22	ABE04993	Human PTHrP, eno
44	49	59.0	175	23	AAO11904	Parathyroid hormone
45	49	59.0	175	23	AAU11908	Parathyroid hormone

ALIGNMENTS

RESULT 1

AAW45879

ID AAW45879 standard; peptide; 16 AA.

AC AAW45879;

XX 30-JUN-1998 (first entry)

DE Peptide membrane binding element.

XX Membrane binding element, thrombotic disease, inflammation;

XX Complement related disease, soluble peptide.

OS Synthetic.

XX WO9802454-A2.

PN 22-JAN-1998.

XX 08-JUL-1997; 97WO-EP03715.

XX 15-JUL-1996; 96GB-0014871.

XX (ADPR-) ADPROTECH PLC.

XX PEG 1, Mossakowska DEI, Smith RAG;

XX WPI; 1994-110524/10.

XX Derivatives of soluble PTHrP, peptide(1-34) bind to low affinity

XX membrane binding groups - useful for treating complement-related and

XX thrombotic diseases, providing improved localisation at cellular

XX membranes

11	65	78.3	17	23	ABB1235	Anti-thrombin, rept
12	58	69.9	20	21	ABE26819	Peptide membrane
13	55	66.3	182	22	AAO3872	Human polypeptide
14	53	63.9	157	22	AAO6556	Human polypeptide
15	52	62.7	119	22	AAO18164	N-terminus of human
16	51	61.4	40	22	AAO33146	Human polypeptide
17	51	61.4	90	21	AAO3790	Human polypeptide
18	51	61.4	117	22	AAO7791	Human polypeptide
19	51	61.4	133	22	AAO10133	Human polypeptide
20	51	61.4	702	22	AAE35147	Human SPAN-1, SEC 1
21	51	61.4	764	22	ABE22230	Novel human diatom
22	51	61.4	894	22	AAE35148	Human NFAP-1, SEC 1
23	51	61.4	946	22	ABE22233	Novel human diatom
24	50	60.2	209	21	AAV95630	Human parathyroid
25	49	59.0	59	22	AAE35897	Human parathyroid
26	49	59.0	79	11	AAE96980	PTHrP, 1-34, peptide
27	49	59.0	101	22	ABE35643	Peptide #2048, eno
28	49	59.0	101	22	ABE24274	Protein #2273, eno
29	49	59.0	101	22	AAE35641	Human PTHrP, eno
30	49	59.0	101	22	AAE35645	Human PTHrP, eno
31	49	59.0	101	22	AAE35647	Peptide #1194, eno
32	49	59.0	101	23	ABE35648	Human PTHrP, eno
33	49	59.0	133	23	AAE23744	Human PTHrP, eno
34	49	59.0	135	23	AAE23745	Human PTHrP, eno
35	49	59.0	139	23	AAE23750	Human PTHrP, eno
36	49	59.0	139	23	AAO14630	Human PTHrP, eno
37	49	59.0	139	23	ABE04991	Human PTHrP, eno
38	49	59.0	141	17	AAE99452	Human PTHrP, eno
39	49	59.0	141	23	AAE23749	Human PTHrP, eno
40	49	59.0	141	23	AAO14631	Human PTHrP, eno
41	49	59.0	141	23	ABE04992	Human PTHrP, eno
42	49	59.0	173	23	AAO14632	Human PTHrP, eno
43	49	59.0	173	22	ABE04993	Human PTHrP, eno
44	49	59.0	175	23	AAO11904	Parathyroid hormone
45	49	59.0	175	23	AAU11908	Parathyroid hormone

Results predicted by chi-square have a
the score of the results being printed,
the total score is 1.000000.

SUMMARY

Accession	Description
AAW45879	Peptide membrane b
ABE26819	Membrane binding e
AAO3872	Anti-thrombotic mem
AAO6556	Wristed/reluctio
AAO18164	Peptide membrane b
AAO33146	Peptide membrane b
AAO3790	Membrane targeted
AAO7791	Membrane binding e
AAO10133	Anti-thrombotic pept
AAE35147	Amino acid sequenc

XX Claim 11, Page 70, 75pp, English.
 XX
 CC The present peptide sequence represents a specifically claimed membrane
 CC binding element. The invention relates to a soluble derivative (A) of a
 CC soluble polypeptide (1), which comprises at least a heterologous
 CC membrane-binding element (MBE) of low membrane affinity covalently
 CC associated with (1). MBE interact, independently and with thermodynamic
 CC additivity, with components of cellular or artificial membranes exposed
 CC to extracellular fluids. (A) are used to treat disorders treatable with
 CC (1) itself, specifically inflammation or any other complement-related
 CC disorder (e.g. neurological disease, graft rejection, myocardial
 CC infarction, sepsis, rheumatoid arthritis and many others; including
 CC application to swelling devices) and thrombolytic disease, but also to
 CC treat allergy, induce weight loss, to treat ischaemia or asthma and as
 CC immunomodulators for treating multiple sclerosis. (A) are administered
 CC orally, typically, by injection or inhalation at 0.01 to 10 (preferably
 CC 0.1 to 10) mg/kg/day.
 XX
 XX Sequence 16 AA,
 SQ
 Query Match 100.0%, Score 81, DB 19, Length 16;
 Best Local Similarity 100.0%, Prod No 1 20-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GSGKSPKPKPKPKPKPK 16
 DB 1 GSGKSPKPKPKPKPKPK 16
 |||||
 RESULT 2
 AAY58856
 ID AAY58856 standard; peptide, 16 AA
 AC AAY58856;
 XX
 DT 08-MAY 2000 (first entry)
 XX
 DE Membrane binding element used in anti-angiogenic polypeptide
 XX
 XX Anti-angiogenic, angiogenesis inhibitor, membrane binding element;
 KW Cancer; tumour; therapy.
 XX
 OS Synthetic.
 XX
 XX W02060604052 A2.
 XX
 PD 27 JAN 2000.
 XX
 XX 16-JUL-1999, 98GB-0615555.
 PF
 PR 16-JUL-1998, 98GB-0615555.
 XX
 XX (ADPR-) ADPR-OTEC PLC.
 PA
 XX Smith RAG, Bright JR, Steward M, Cox VF,
 FI WPI, 2000 471498/50.
 XX
 XX The present sequence is a claimed example of a lysine-rich peptidic
 CC membrane binding element (MBE) that can be utilised in novel
 CC soluble derivatives (1) of anti-angiogenic polypeptides of the
 CC invention. (1) comprise 3 or more heterologous MBEs with low
 CC membrane affinity that are covalently attached to a soluble
 CC anti-angiogenic polypeptide such as a non-catalytic region of human
 CC plasminogen, fragments of related proteins containing kringle
 CC domains, fragments of collagen or prolactin, neutralising
 CC

CC antibodies against receptors for angiogenic mediators, and
 CC antagonists of integrins involved in angiogenesis. The MBEs
 CC interact independently with thermodynamic additivity, with
 CC components of the vascular endothelium (1) provide targeted
 CC delivery of the anti-angiogenic polypeptide to cell membranes and
 CC sites of active angiogenesis, particularly the vascular endothelium,
 CC and therefore increase the local concentration and reduce the risk
 CC of adverse effects on normal processes elsewhere in the vasculature.
 CC They are used in a claimed method of treatment of primary or
 CC secondary tumour.
 XX
 XX Sequence 16 AA;
 SQ
 Query Match 100.0%, Score 81, DB 21, Length 16;
 Best Local Similarity 100.0%, Prod No 1 20-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GSGKSPKPKPKPKPKPK 16
 DB 1 GSGKSPKPKPKPKPKPK 16
 |||||
 RESULT 3
 ABB81238
 ID ABB81238 standard; peptide, 16 AA.
 XX
 AC ABB81238;
 XX
 DT 20-AUG 2002 (first entry)
 XX
 DE Antibacterial membrane binding peptide SEQ ID NO:5.
 XX
 XX Antibacterial, glycopeptide, peptidic membrane associating element;
 KW Bacterial infection, vancomycin, peptidoglycan biosynthesis inhibition;
 KW antibiotic.
 XX
 OS Synthetic.
 XX
 XX W0000000412-A1.
 XX
 XX 10 MAY 2002.
 XX
 XX 02-NOV-2001; 2001WO-0504857
 DP
 XX 03-NOV 2000; 2000EP 0026034.
 PP
 XX (UVCA) UNIV CAMBRIDGE TECH SPEVTECH LTD.
 PA (ADPP-) ADPP-OTEC LTD.
 XX
 XX Cooper MA, Berley JP;
 DT WPI, 2002 471498/50.
 XX
 XX Antibacterial compound, useful for the treatment of a bacterial
 XX infection by e.g. gram positive or negative bacteria, comprises a
 XX conjugate of glycopeptide and a peptidic membrane associating element
 XX Claim 7, Page 57, 64pp; English.
 XX
 XX The present invention describes an antibacterial compound (1), comprising
 CC a conjugate of glycopeptide and peptidic membrane associating elements,
 CC (1) comprises the formula V-L-W-X where: V is a glycopeptide moiety that
 CC inhibits peptidoglycan biosynthesis in bacteria; L is a linking group;
 CC W is a peptidic membrane associating element; and X is H or a membrane
 CC insertive element. Also described: (1) a method of treating or preventing
 CC a bacterial infection, comprising the administration of (1); and (2) use
 CC of (1) in the manufacture of a medicament for the treatment or prevention
 CC of a bacterial infection. (1) are used in the manufacture of a medicament
 CC for the treatment or prophylaxis of a bacterial infection in a human or
 CC animal body, including both the gram positive and gram negative bacteria
 CC including *Mycobacterium* sp., *Enterococcus* sp., *Borrelia* sp., *Plasmodium*
 CC *Staphylococcus* sp., *Vibrio* sp., *Neisseria* sp., *Aspergillus* sp.,
 CC sp., *Hemophilus* sp., *Chlamydia* sp., *Pseudomonas* sp., *Acinetobacter* sp.,

CC The present peptide sequence represents a specifically claimed membrane binding element. The invention relates to a soluble derivative (A) of a soluble polypeptide (1), which comprises at least 2 heterologous membrane-binding elements (MBE) of low membrane affinity covalently associated with (1). MBE interact, independently and with thermodynamic additivity, with components of cellular or artificial membranes exposed to extracellular fluids. (A) are used to treat disorders treatable with (1) itself, specifically inflammation or any other complement-related disorder (e.g. neurological disease, graft rejection, myocardial infarction, sepsis, rheumatoid arthritis and many others, including application to indwelling devices) and thrombolytic disease, but also to treat allergy, induce weight loss, to treat ischaemia or asthma and as immuno-modulators for treating multiple sclerosis. (A) are administered orally, topically, by injection or inhalation at 0.01-10 (preferably 0.1-10) mg/kg/day.

CC Sequence 17 AA:
Query Match 100.00; Score 81; PP 10; Length 17;
Best Local Similarity 100.00; Prod No 1.3e-05; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GSSKSPSPKYYKPPGD 16
| | | | | | | | | | | | | | | | | |
Db 1 GSSKSPSPKYYKPPGD 16

RESULT 6
ID AAW45891 standard; peptide; 17 AA.
AC AAW45891;
XX
XX
DT 30-JUN-1998 (first entry)
XX
DE Peptide membrane binding element.
XX
KW Membrane binding element; thrombotic disease, soluble protein.
KW Complement related disease, integral membrane protein, inflammation.
XX
XX Synthetic.
XX WC5802547-A2.
PN 20 JAN 1998.
XX
FD 08-JUL-1997; 97WO-BP03715.
XX
PP 15-JUL-1996; 96GB-0014871.
XX
XX (ADPR-) ADPROTECH PLC.
XX
XX Dodd I, Mossakowska DEI, Smith RAG,
PI WPI; 1998-110524/10
XX
XX Derivatives of soluble polypeptide(s) bonded to low affinity
PT membrane binding groups - useful for treating complement related and
PT thrombotic diseases, providing improved localisation at cellular
PT membranes
XX
XX Claim 21, page 71, 75pp, English.

CC The present peptide sequence represents a specifically claimed membrane binding element. The invention relates to a soluble derivative (A) of a soluble polypeptide (1), which comprises at least 2 heterologous membrane-binding elements (MBE) of low membrane affinity covalently associated with (1). MBE interact, independently and with thermodynamic additivity, with components of cellular or artificial membranes exposed to extracellular fluids. (A) are used to treat disorders treatable with (1) itself, specifically inflammation or any other complement-related disorder (e.g. neurological disease, graft rejection, myocardial infarction, sepsis, rheumatoid arthritis and many others, including

CC application to indwelling devices) and thrombolytic disease, but also to treat allergy, induce weight loss, to treat ischaemia or asthma and as immuno-modulators for treating multiple sclerosis. (A) are administered orally, topically, by injection or inhalation at 0.01-10 (preferably 0.1-10) mg/kg/day.

CC Sequence 17 AA:
Query Match 100.00; Score 81; PP 10; Length 17;
Best Local Similarity 100.00; Prod No 1.3e-05; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GSSKSPSPKYYKPPGD 16
| | | | | | | | | | | | | | | | | |
Db 1 GSSKSPSPKYYKPPGD 16

RESULT 7
ID AAB26818 standard; peptide; 17 AA.
XX
AC AAB26818;
XX
XX
DT 23-JAN 2001 (first entry)
XX
DE Membrane targeted complement inhibitor peptide.
XX
DE Cation perfuser, transferrin, storage, anti-inflammatory;
KW immunosuppressive, vasoparic, complement activation inhibitor;
KW allergic rejection; ischaemia reperfusion injury.
XX
XX Synthetic.
XX
XX Key/ Location/Qualifiers
XX Modified-site 17
XX /note- "C-terminal Cys forms a disulphide bond with the
PT C-terminal Cys of protein AAB26817"
PT
PT W02000053007-A1
XX
XX 14-SEP-2000.
XX
XX 09-MAP 2000; 2000WO-0200834.
XX
XX 10-MAP-1000; 0009-0005503.
XX
XX (ADPR-) ADPROTECH LTD.
XX
XX Smith RAG, Pratt JP, Sacks SH;
DE WPI; 2000 601900/57.
XX
XX
XX Preparation for perfusing organ prior to transplantation or storage
PT comprises soluble derivative of a soluble polypeptide which comprises
PT two heterologous membrane binding elements with low membrane affinity
PT
XX
XX Example 1; Page 40, 47pp, English.

CC The present invention relates to formulations and preparations for perfusing an organ prior to transplantation or storage. The preparation comprises a soluble derivative of a polypeptide, which has two or more heterologous membrane binding elements. The membrane binding elements are capable of interaction, independently and with thermodynamic additivity, with membrane components of the organ exposed to extracellular perfusion fluids, and a flush storage solution. The preparation exhibits anti-inflammatory, immunosuppressive and vasoparic activity and works as a complement activity inhibitor and an inhibitor of white blood cell lymphocyte activity. The preparation is used for preparing an organ prior to transplantation or storage and for prevention treatment or amelioration of a disease or disorder associated with inflammation, inappropriate complement activation or inappropriate activation of coagulant or thrombotic processes prior to, during or after

to drain the pleural space. It is useful for pleural resection of irradiated organs in thoracic ischaemic necrosis or injury in thoracic aortic aneurysm resection. The pleural resection and thoracic resection. The pleural resection and thoracic resection. The pleural resection and thoracic resection.

Model 83; DB 21; 100000000	
Prod. No. 1.3e-05	
Matches	0
Capacities	0

22

THE CONCEPT OF THE "WELL-BEING" OF THE PEOPLE

[illegible]

P

$$\begin{aligned} &= \\ &= \\ &= \\ &= \\ &= \\ &= \\ &= \end{aligned}$$

VENUE

an aromatic polyamide, the material for
my fingers, sent this material by attached
it to me.

— *pro*

[illegible]

an alternative to, or in conjunction with, antibiotic prophylaxis. (1) has stronger binding to bacterial membranes which have a higher potential for acidic phospholipids than the eukaryotic organisms, also having a higher penetration of membrane associated biosynthetic proteins. Vancospen shows an enhanced antimicrobial activity upon derivatization with (1) and is effective to treat the antibiotic resistant bacterial strains. ABB81234 to ABB81235 represent peptides given in the exemplification of the present invention.

XX Sequence 17 AA;

Query Match 100.0%, Score 63, DP 22, Length 17;

Best Local Similarity 100.0%, Pred. No. 1.3e-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSSKSPSKYKXKPGD 16

DB 1 GSSKSPSKYKXKPGD 16

RESULT 10

ABB07533

ID ABB07533 standard; peptide; 17 AA

XX AC ABB07533;

XX DT 22 APR 2002 (first entry)

XX DE Amino acid sequence of APT542.

XX EW CD59; lipid raft derivative; NAF; neuroprotective; nontropic; human;

XX EW ceramiprotective; ceripathogenic; anti-allergic; antileuk; cardiac;

XX EW antipsoriasis; antiaesthetic; dermatological; hypertensive; vasotropic;

XX EW antirheumatic; antiarthritic; antiinflammatory; ophthalmological;

XX EW immunosuppressive; antianemic; nephrotropic; antiinfertility;

XX EW antibacterial; antiatherosclerotic; vulvetry;

XX OS Synthetic.

XX OS Homo sapiens.

XX Key Location/Qualifiers

XX Modified-site 1

XX /note- "N myristoyl"

XX Modified-site 17

XX /note- "C-terminal 2-thiopyridyl-1-OR2"

XX W02000448-A1.

XX 17-JAN-2002.

XX 06-JUL 2001, 2001W03504867.

XX 07-JUL 2000, 2000J0304211.

XX (ADPR-) ADPR07533 LTD.

XX Rowling PJE, Smith GP, Ridley SH;

XX WPI; 2002 164846/21.

XX Lipid raft targeted derivative of a soluble polypeptide e.g. a soluble

XX complement regulatory molecule for treating disorders involving

XX complement activity and various inflammatory, neurological and immune

XX disorders

XX Example 1, Page 43, 51pp, English.

XX The invention relates to a soluble derivative (1) of a soluble

XX polypeptide (17) has two or more heterogeneous membrane binding elements

XX with low membrane affinity covalently associated with the polypeptide,

XX the elements being capable of interacting with components of cellular or

XX artificial membranes exposed to extracellular fluids and target lipid

XX raft components of membrane (17) is useful for treating disorders

XX

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amenable to treatment by a soluble peptide fragment of CD59, NAF or other therapeutic agent, and for the preparation of a medicament for treatment of disorders involving complement activity and various inflammatory and immune disorders. (1) is useful for treating neurological disorders (e.g. multiple sclerosis, stroke, Parkinson's, Alzheimer's disease, traumatic brain injury and allergic encephalitis), disorders of inappropriate or undesirable complement activation (e.g. xenograft rejection, corneal graft rejection), inflammatory disorders (including ulcerative colitis, Crohn's disease, uveitis, psoriasis, asthma, scleroderma, acute pancreatitis), post-ischemic reperfusion conditions (e.g. myocardial infarction, hypertension, renal ischaemia, restenosis, atherosclerosis), infectious diseases or sepsis (e.g. multiple organ failure, septic shock), autoimmune diseases (e.g. rheumatoid arthritis, systemic lupus erythematosus, hemolytic anemia, glomerulonephritis and myasthenia gravis), reproductive disorders (antibody or complement mediated infertility), and wound healing. The present sequence represents the amino acid sequence of APT542, used in the synthesis of a lipid raft targeted derivative of soluble human urinary CD59 (APT532).

XX Sequence 17 AA;

Query Match 100.0%, Score 63, DP 22, Length 17;

Best Local Similarity 100.0%, Pred. No. 1.3e-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSSKSPSKYKXKPGD 16

DB 1 GSSKSPSKYKXKPGD 16

RESULT 11

ABB81235

ID ABB81235 standard; peptide; 17 AA

XX AC ABB81235;

XX DT 22 AUG 2002 (first entry)

XX DE Antibacterial peptide SEQ ID NO:2.

XX EW Antibacterial; glycopeptide; peptidic membrane associating element;

XX EW Eukaryotic infection; vancomycin; peptidoglycan biosynthesis inhibition;

XX EW antibiotic.

XX OS Synthetic.

XX W0200036612-A1.

XX 10 MAY 2002.

XX 02 NOV 2001; 2001W03504867.

XX 02 NOV 2000; 2000J0304211.

XX (UYCA) UNIV CAMBRIDGE TECH SERVICES LTD.

XX (ADPR-) ADPR07533 LTD.

XX Cooper MA, Betley JR,

XX WPI; 2002-471498/50.

XX Antibacterial compound, useful for the treatment of a bacterial

XX infection by a gram positive or negative bacterium, comprising a

XX conjugate of glycopeptide and peptidic membrane associating element

XX Example 4; Page 52; 64pp; English.

XX The present invention describes an antibacterial compound (1), comprising

XX a conjugate of glycopeptide and peptidic membrane associating elements,

XX (1) comprises the formula V-H-W-X, where: V = a glycopeptide moiety that

XX inhibits peptidoglycan biosynthesis in bacteria; W = a linking group;

XX W = a peptidic membrane associating element; and X = H or a membrane-

XX insertive element. Also described: (i) a method of treating or preventing

XX

XX

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XX

the administration of (1) and (2) use a medicament for the treatment or prevention of a bacterial infection in a human or animal. The medicament comprises a bactericidal agent and a bacteriostatic agent. The bactericidal agent is a peptide which is a derivative of a polypeptide, which has two or more heterologous membrane binding elements, the peptide binding elements are capable of interacting, independently and with thermodynamic advantage, with membrane components of the organ exposed to extracellular infection fluids, and a flush storage solution. The preparation exhibits anti-inflammatory, immunosuppressive and vasoactive activity and a high as a complement activator. The preparation is used for preparing an organ prior to transplantation or storage and for prevention, treatment or amelioration of a disease or disorder associated with inflammation, infection or thrombotic processes prior to, during or after transplantation or storage of an organ. The preparation is useful for treating hyperacute and acute allograft rejection of transplanted organs such as kidney, heart, liver or lungs, ischaemia-reperfusion injury in transplanted organs, xenograft rejection and corneal graft rejection. The present sequence represents a peptidic membrane binding element used in an example of the preparation of the invention.

Query Match 69.9%; Score 58; ID 21; Length 27;
Best Local Similarity 100.0%; Pred. No. 3,567;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SPSKVKKVKYKPG 15
DB 2 SPSKVKKVKYKPG 12
|||||
|||||

AA

BB

Human polypeptide SEQ ID NO 17764.
Human, cytokine, cell proliferation, cell differentiation, bone therapy;
vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorders; arthritis; inflammation.

CC

DDally N Myristoyl Gly

DDally S 2 Thiopyridyl Gly NH₂

EE

Isolated nucleic acids and polypeptides, useful for preventing
diagnosing and treating e.g. leukaemia, inflammation and immune
disorders -
Claim 20; SEQ ID NO 17764; 1399pp + Sequence listing; English.

Example 2; Page 20; 47pp - English.

The present invention relates to formulations and preparations for perfusing an organ prior to transplantation or storage. The preparation comprises a soluble derivative of a polypeptide, which has two or more heterologous membrane binding elements. The membrane binding elements are capable of interacting, independently and with thermodynamic advantage, with membrane components of the organ exposed to extracellular infection fluids, and a flush storage solution. The preparation exhibits anti-inflammatory, immunosuppressive and vasoactive activity and a high as a complement activator. The preparation is used for preparing an organ prior to transplantation or storage and for prevention, treatment or amelioration of a disease or disorder associated with inflammation, infection or thrombotic processes prior to, during or after transplantation or storage of an organ. The preparation is useful for treating hyperacute and acute allograft rejection of transplanted organs such as kidney, heart, liver or lungs, ischaemia-reperfusion injury in transplanted organs, xenograft rejection and corneal graft rejection. The present sequence represents a peptidic membrane binding element used in an example of the preparation of the invention.

Sequence 20 AA;

Query Match 69.9%; Score 58; ID 21; Length 27;
Best Local Similarity 100.0%; Pred. No. 3,567;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SPSKVKKVKYKPG 15
DB 2 SPSKVKKVKYKPG 12
|||||
|||||

RESULT 13

AAO03872
ID AAO03872 standard; Protein; 83 AA.

XX

AC AAO03872;

DT 06-NOV-2001 (first entry)

XX Human polypeptide SEQ ID NO 17764.

Human, cytokine, cell proliferation, cell differentiation, bone therapy;
vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorders; arthritis; inflammation.

XX Homo sapiens.

XX W0200164835-A2.

XX 07-SEP-2001.

XX 26-FEB-2001, C061W 03-10-01.

XX 28-FEB-2000; 2000US-0511126.

XX 18-MAY-2000; 2000US-0574399.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-514835/56.

XX N-PSDB; AA183803.

Isolated nucleic acids and polypeptides, useful for preventing
diagnosing and treating e.g. leukaemia, inflammation and immune
disorders -

Claim 20; SEQ ID NO 17764; 1399pp + Sequence listing; English.

QY 1 GSSGSPSXXXXX 13
|||:|||||
Db 106 GSSPNPXXXX 118

Search completed: March 3, 2003, 10:18:17
Job time : 29.878 secs


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DB 145 SPSNETPPKPPKPPKPPK 163
|||||
US-08-405-175A-6
RESULT 2
Sequence 6, Application US/08405175A
Patent No. 5885772
GENERAL INFORMATION:
APPLICANT: Aderem, Alan A.
APPLICANT: Chen, Jianmin
APPLICANT: Chang, Sandy
TITLE OF INVENTION: METHOD FOR THE DETECTION OF AMENGEHALLY
NUMBER OF SEQUENCES: 12
REFERENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08405175A
APPLICATION NUMBER: US/08405175A
FILING DATE: 16-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jack E. Esli, David A.
REGISTRATION NUMBER: 26,742
REFERENCE/AGENT NUMBER: 435 121A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Predicted primary structure of aminoglycoside
HYPOTHETICAL: NO
US-08-405-175A-7
Query Match 94.0%, Score 99, DP 2, Length 309
Best Local Similarity 100.0%, Freq. No. 7, 67
Matches 19: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 139 SPSNETPPKPPKPPKPPK 156
|||||
US-08-405-175A-8
RESULT 4
Sequence 9, Application US/08405175A
Patent No. 5885772
GENERAL INFORMATION:
APPLICANT: Aderem, Alan A.
APPLICANT: Chen, Jianmin
APPLICANT: Chang, Sandy
TITLE OF INVENTION: METHOD FOR THE DETECTION OF AMENGEHALLY
NUMBER OF SEQUENCES: 12
REFERENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08405175A
APPLICATION NUMBER: US/08405175A
FILING DATE: 16-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jack E. Esli, David A.
REGISTRATION NUMBER: 26,742
REFERENCE/AGENT NUMBER: 435 121A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
DB 144 SPSNETPPKPPKPPKPPK 162
|||||
US-08-405-175A-7
RESULT 3
Sequence 7, Application US/08405175A
Patent No. 5885772
GENERAL INFORMATION:
APPLICANT: Aderem, Alan A.
APPLICANT: Chen, Jianmin
APPLICANT: Chang, Sandy
TITLE OF INVENTION: METHOD FOR THE DETECTION OF AMENGEHALLY
NUMBER OF SEQUENCES: 12
REFERENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey

```

US-08-405-175A-3

Sequence 3, Application US/89405175A

Patent No. 5885772

GENERAL INFORMATION:

APPLICANT: Aderem, Alan A.

APPLICANT: Chen, Jianmin

APPLICANT: Chang, Sandy

TITLE OF INVENTION: METHOD FOR THE DETECTION OF ANTERIOR

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-POS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA

APPLICATION NUMBER: US/89/405,175A

FILING DATE: 16-MAR-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 630-1-121A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS

LENGTH: 199 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

DESCRIPTION: rabbit alveolar macrophage Mac-2APR65

US-08-405-175A-3

Query Match 58.7%

Best Local Similarity 64.7%

Score 61; DB 2; Length 199;

Pat. No. 5,895;

Matches 11; Conservative 2; Mismatches 4; Indels 1; Gaps 0;

QY 1 SPSPNTPKPKPKPKPKPKPK 17

DB 80 APPETPNPKPKPKPKPKPK 96

US-08-818-253-26

Sequence 26, Application US/08818253

Patent No 5998204

GENERAL INFORMATION:

APPLICANT: Tsien, Roger Y.

APPLICANT: Miyawaki, Atsushi

TITLE OF INVENTION: FLUORESCENT PROTEIN GLNSRPS FOR

TITLE OF INVENTION: DETECTION OF ANALYTES

NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

US-09-214-913-39.ra1

Sequence 3, Application US/89405175A

Patent No. 5885772

GENERAL INFORMATION:

APPLICANT: Aderem, Alan A.

APPLICANT: Chen, Jianmin

APPLICANT: Chang, Sandy

TITLE OF INVENTION: METHOD FOR THE DETECTION OF ANTERIOR

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-POS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA

APPLICATION NUMBER: US/89/405,175A

FILING DATE: 16-MAR-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 630-1-121A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS

LENGTH: 199 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

DESCRIPTION: rabbit alveolar macrophage Mac-2APR65

US-08-405-175A-3

Query Match 58.7%

Best Local Similarity 64.7%

Score 61; DB 2; Length 199;

Pat. No. 5,895;

Matches 11; Conservative 2; Mismatches 4; Indels 1; Gaps 0;

QY 1 SPSPNTPKPKPKPKPKPKPK 17

DB 80 APPETPNPKPKPKPKPKPK 96

US-08-818-253-26

Sequence 26, Application US/08818253

Patent No 5998204

GENERAL INFORMATION:

APPLICANT: Tsien, Roger Y.

APPLICANT: Miyawaki, Atsushi

TITLE OF INVENTION: FLUORESCENT PROTEIN GLNSRPS FOR

```

; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/018,253
; FILING DATE: 14-MAR-1997
; FILER APPLICATION NUMBER
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Baile, Ph D., Lisa A.
; REGISTRATION NUMBER: 38,147
; REFERENCE/OPFFET NUMBER: 07/07/944001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/678-5070
; TELEFAX: 617/678-5070
; INFORMATION FOR SEQ ID NO. 1:
; SEQUENCE: HANA-TELESTIN
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-018-253-25

```

```

Query Match: 57.7%; Seq-ID: 60, EP 4, Length 25;
Best Local Similarity: 100.0%; Pred. No. 0.018;
Matches: 12; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

```

```

CY 9 KKKKKKKKKKKK 19
DB 1 KKKKKKKKKKKK 12

```

RESULT 8

```

US-08-018-253-25
; Sequence 25, Application US/08/018,253
; Patent No. 6376257
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES
; FILE REFERENCE: 07257/042001
; CURRENT APPLICATION NUMBER: US/08/018,253B
; CURRENT FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 25
; TYPE: PPT
; ORGANISM: Rattus norvegicus
US-08-018-253-25

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Query Match: 57.7%; Seq-ID: 60, EP 4, Length 25;
Best Local Similarity: 100.0%; Pred. No. 0.018;
Matches: 12; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

```

```

CY 9 KKKKKKKKKKKK 19
DB 1 KKKKKKKKKKKK 12

```

RESULT 9

```

US-08-018-322-20
; Sequence 20, Application US/08/018,322
; Patent No. 6376257
; GENERAL INFORMATION:
; APPLICANT: Persechini, Anthony
; TITLE OF INVENTION: DETECTION BY FEET CHANGES OF LIGAND
; TITLE OF INVENTION: BINDING BY GFE FINGER PROTEINS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENT ADDRESS:
; ADDRESS: NIKON, HARGRAVE, DEVANS & DOYLE LLP
; STREET: Clinton Square, P.O. Box 1051

```

```

; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Batchin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/040,100
; FILING DATE:
; CLASSIFICATION: 43C
; ATTORNEY/AGENT INFORMATION:
; NAME: BRAMAN, SUSAN J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/OPFFET NUMBER: 17/060170
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 715-263-1636
; TELEFAX: 715-263-1600
; INFORMATION FOR SEQ ID NO. 20
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-040-100-20

```

```

Query Match: 57.7%; Seq-ID: 60, EP 4, Length 25;
Best Local Similarity: 100.0%; Pred. No. 0.018;
Matches: 12; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

```

```

CY 8 KKKKKKKKKKKK 19
DB 1 KKKKKKKKKKKK 12

```

RESULT 10

```

US-09-316-919-42
; Sequence 42, Application US/09/316,919
; Patent No. 6469154
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Baird, Geoffrey
; TITLE OF INVENTION: FLUORESCENT PROTEIN INDICATORS
; FILE REFERENCE: 07257/073001
; CURRENT APPLICATION NUMBER: US/09/316,919
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 25
; TYPE: PPT
; ORGANISM: Rattus norvegicus
US-09-316-919-42

```

```

Query Match: 57.7%; Seq-ID: 60, EP 4, Length 25;
Best Local Similarity: 100.0%; Pred. No. 0.018;
Matches: 12; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

```

```

CY 8 KKKKKKKKKKKK 19
DB 1 KKKKKKKKKKKK 12

```

RESULT 11

```

US-08-405-175A-4
; Sequence 4, Application US/08/405,175A
; Patent No. 585772
; GENERAL INFORMATION:
; APPLICANT: Aderem, Alan A.
; APPLICANT: Chen, Jianmin

```

THE DETECTION OF ANOMALY

NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 08,347
REFERENCE/DOCKET NUMBER: 07257/043001
TELEPHONE: 619/678-5099
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS
LENGTH: 24 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-818-253-27

Query Match 46.2% Score 48; DB 2; Length 24;
Best Local Similarity 90.0% Pred. No. Gaps: 0;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 KKKKPSFY 18
DB 1 KKKKPSFY 10

RESULT 13
US-08-818-252-27
Sequence 27, Application US/08818252B
Patent No. 6197928
GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: FLORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: DETECTION OF ANALYTES
FILE REFERENCE: 07257/043001
CURRENT APPLICATION NUMBER: US/08818252B
CURRENT FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 27
LENGTH: 24
TYPE: PRT
ORGANISM: Mus musculus
US-08-818-252-27

Query Match 46.2% Score 48; DB 4; Length 24;
Best Local Similarity 90.0% Pred. No. Gaps: 0;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 KKKKPSFY 18
DB 1 KKKKPSFY 10

RESULT 14
US-08-842-322-21
Sequence 21, Application US/08842322
Patent No. 6176257
GENERAL INFORMATION:
APPLICANT: Persechini, Anthony
TITLE OF INVENTION: DETECTION BY FREQUENCY CHANGES OF LIGAND
TITLE OF INVENTION: BINDING BY GEL FUSION EXPERIMENTS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESS: NIXON, HARVEY, DEANE & DYER LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

NT PROTEIN SENSOR

US Version 2.0b

US Version 2.0b

```

; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/942,322
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: BRAMAN, SUSAN J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/EXAMINER NUMBER: 176/00170
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1636
; TELEFAX: 716-263-1600
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-942,322 21

```

```

Query Match          46.2%; Score 48; DB 4; Length 24;
Best Local Similarity 90.0%; Pred. No. 0.91;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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```

QY 9 KKKKFSKK 18
Db 1 KKKKFSKK 10

```

```

RESULT 15
US 09-214-919-43
; Sequence 43, Application US/09316919
; Patent No. 6469154
; GENERAL INFORMATION:
; APPLICANT: Tshen, Roger Y.
; APPLICANT: Baird, Geoffrey
; TITLE OF INVENTION: FLUORESCENT PROTEIN INDICATORS
; FILE REFERENCE: 07257/073001
; CURRENT APPLICATION NUMBER: US/09/316,919
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-214-919-43

```

```

Query Match          46.2%; Score 48; DB 4; Length 24;
Best Local Similarity 90.0%; Pred. No. 0.91;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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```

QY 9 KKKKFSKK 18
Db 1 KKKKFSKK 10

```

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Search completed: March 3, 2003, 06:15:50
Job time : 14.6829 secs

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Version 5.1.3
4 2003 CompuGen Inc.
Search (without alignment)
117,657 Mbits with updates/sec

122 residues
non parameters: 100000

Results predicted by chance have a
score of the result being printed,
the total score distribution is:

SUMMARY

Accession	Description
histone H2B.IV - V	
W09G12.7	
hypothetical prote	
kidney - kidney	
hypothetical prote	
exchanging	
signal recognition	
proteasome reg	
hypothetical prote	
histone H2B.III -	
protein VP2 -	
amino acid	
terminal domain	
histone H1, gerad	
hypothetical prote	
AMP gated chann	
AMP gated ion cha	
repetitive nucleor	
hypothetical prote	
single-strand DNA/	
polymerase protein	
histone H1, gerad	
AMP translocation	
hypothetical prote	
specific his	
histone H1-2 (vali	
histone H1d - rat	
histone H1-4 (vali	
hypothetical prote	

30	45	54.9	430	2	T46099	hypothetical prote
31	45	54.9	440	2	S74197	ATP dependent 26S
32	45	54.9	482	2	T17250	hypothetical prote
33	45	54.9	520	2	S61193	hypothetical prote
34	45	54.9	756	2	T05829	hypothetical prote
35	45	54.9	796	2	C85220	hypothetical prote
36	45	54.9	967	2	G86229	hypothetical prote
37	45	54.9	1056	2	E96748	hypothetical prote
38	44.5	54.3	704	2	S33263	transcription init
39	44	53.7	51	2	F10069	histone H1 seed
40	44	53.7	142	2	S54481	hypothetical prote
41	44	53.7	192	2	T31532	hypothetical prote
42	44	53.7	212	2	A28470	histone H1 mouse
43	44	53.7	219	2	C69948	phase related prot
44	44	53.7	221	2	S42492	histone H1 mouse
45	44	53.7	250	2	S49156	HapC localization

ALIGNMENTS

RESULT 1
JQ0797
histone H2B.IV - Volvox carteri
C:Species: Volvox carteri
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 12-Feb-1993
C:Accession: JQ0797
R:Mueller, K.; Lindauer, A.; Bruederlein, M.; Schmitt, R.
Gene 93, 167-175, 1990
A:Title: Organization and transcription of Volvox histone encoding genes: similarities
A:Reference number: JQ0794; MJD:9103324; PMID:2227431
A:Accession: JQ0797
A:Molecule type: DNA
A:Residues: 1-155 <MUE>
A:Cross-references: GB:M31922; NID:910657; EID:AA3450.1; FID:H17769
C:Genetics:
A:Gene: H2B-IV
C:Superfamily: histone H2B
C:Keywords: chromatin, histone, DNA binding, nucleosome core, nucleos

Query Match 62.2%; Score 51; DB 2; Length 156;
Best Local Similarity 69.3%; Pred. No. 4.1;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 7;
CY 3 PPKYKYSKSS 15
DB 29 PPKYKYPAPYS 41
RESULT 2
G88636
Protein W09G12.7 (imported) - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: G88636
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2019, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for genomic and molecular biology
A:Reference number: A75000; MJD:900000; PMID:955516
A:Note: See website: genome.wisc.edu/celegans/ and www.sanger.ac.uk/Projects/CE for
A:Note: Published errata appeared in Science 281, 15, 1999; Science 283, 2103, 1999; and
A:Accession: G88636
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-369 <STO>
A:Cross-references: GB:chr.IV; FID:AA004417.1; FID:3211892; NID:910657; EID:AA3450.1; FID:H17769
C:Genetics:
A:Gene: W09G12.7
A:Map position: 4

Query Match 62.2%; Score 51; DB 2; Length 156;
Best Local Similarity 73.3%; Pred. No. 4.5;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 7;
CY 3 PPKYKYSKSS 15
DB 29 PPKYKYPAPYS 41


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-- version 5.1.3
-- 2002 Copyright 2002

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[illegible]

100

Variable	Search for new records	Wipe out old records	Update records/sec
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1.4	1.0	1.0	1.0
1.5	1.0	1.0	1.0
1.6	1.0	1.0	1.0
1.7	1.0	1.0	1.0
1.8	1.0	1.0	1.0
1.9	1.0	1.0	1.0
2.0	1.0	1.0	1.0
2.1	1.0	1.0	1.0
2.2	1.0	1.0	1.0
2.3	1.0	1.0	1.0
2.4	1.0	1.0	1.0
2.5	1.0	1.0	1.0
2.6	1.0	1.0	1.0
2.7	1.0	1.0	1.0
2.8	1.0	1.0	1.0
2.9	1.0	1.0	1.0
3.0	1.0	1.0	1.0
3.1	1.0	1.0	1.0
3.2	1.0	1.0	1.0
3.3	1.0	1.0	1.0
3.4	1.0	1.0	1.0
3.5	1.0	1.0	1.0
3.6	1.0	1.0	1.0
3.7	1.0	1.0	1.0
3.8	1.0	1.0	1.0
3.9	1.0	1.0	1.0
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4.1	1.0	1.0	1.0
4.2	1.0	1.0	1.0
4.3	1.0	1.0	1.0
4.4	1.0	1.0	1.0
4.5	1.0	1.0	1.0
4.6	1.0	1.0	1.0
4.7	1.0	1.0	1.0
4.8	1.0	1.0	1.0
4.9	1.0	1.0	1.0
5.0	1.0	1.0	1.0
5.1	1.0	1.0	1.0
5.2	1.0	1.0	1.0
5.3	1.0	1.0	1.0
5.4	1.0	1.0	1.0
5.5	1.0	1.0	1.0
5.6	1.0	1.0	1.0
5.7	1.0	1.0	1.0
5.8	1.0	1.0	1.0
5.9	1.0	1.0	1.0
6.0	1.0	1.0	1.0
6.1	1.0	1.0	1.0
6.2	1.0	1.0	1.0
6.3	1.0	1.0	1.0
6.4	1.0	1.0	1.0
6.5	1.0	1.0	1.0
6.6	1.0	1.0	1.0
6.7	1.0	1.0	1.0
6.8	1.0	1.0	1.0
6.9	1.0	1.0	1.0
7.0	1.0	1.0	1.0
7.1	1.0	1.0	1.0
7.2	1.0	1.0	1.0
7.3	1.0	1.0	1.0
7.4	1.0	1.0	1.0
7.5	1.0	1.0	1.0
7.6	1.0	1.0	1.0
7.7	1.0	1.0	1.0
7.8	1.0	1.0	1.0
7.9	1.0	1.0	1.0
8.0	1.0	1.0	1.0
8.1	1.0	1.0	1.0
8.2	1.0	1.0	1.0
8.3	1.0	1.0	1.0
8.4	1.0	1.0	1.0
8.5	1.0	1.0	1.0
8.6	1.0	1.0	1.0
8.7	1.0	1.0	1.0
8.8	1.0	1.0	1.0
8.9	1.0	1.0	1.0
9.0	1.0	1.0	1.0
9.1	1.0	1.0	1.0
9.2	1.0	1.0	1.0
9.3	1.0	1.0	1.0
9.4	1.0	1.0	1.0
9.5	1.0	1.0	1.0
9.6	1.0	1.0	1.0
9.7	1.0	1.0	1.0
9.8	1.0	1.0	1.0
9.9	1.0	1.0	1.0
10.0	1.0	1.0	1.0

1

100
90
80
70
60
50
40
30
20
10
0

SC-100

1. The predicted score is 1.00. Have a
 2. The score of the result being printed,
 3. The total score for the item.

SEI BURNING

Division

[illegible]

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RESULT 1
SR14 CANFA
ID SR14 CANFA STANDARD; PRT: 110 AA.
AC P1655, Q28277,
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Signal recognition particle 14 kDa protein (SRP14).
GN SRP14.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Canidae; Canis.
OX NCBI_TaxID=9615;
(1) _RN
(1) _RN
SEQUENCE FROM N.A.
Baugh, C.; Wilson, C.;
Submitted 1990-11-02 to the EMBL/GenBank/DBJ databases.
(2)
SEQUENCE OF 14-95 FROM N.A., AND SEQUENCE OF 2-19 AND 77-95
FROM N.A.
REF TISSUE:Kidney;
MEDLINE=90069341; PubMed=2557425;
RX

```

Strub K., Walter P.:
"Isolation of a cDNA clone of the 14-kDa subunit of the signal
recognition particle by cross-hybridization of differentially primed
polymerase chain reactions.";
Proc. Natl. Acad. Sci. U.S.A. 86(7/4):975(1989).
FUNCTION SIGNAL RECOGNITION PARTICLE ASSEMBLY HAS A CRITICAL ROLE
IN TARGETING SECRETORY PROTEINS TO THE ER LUMEN ENDOPLASMIC RETICULUM
MEMBRANE. SRP9 TOGETHER WITH SRP14 AND THE ALD PROTEIN OF THE SRP
RNA, CONSTITUTES THE RECOGNITION AND FIRST LAYERS OF SRP RNA BINDING.
OF SRP9 AND SRP14 IS REQUIRED FOR SRP RNA BINDING.
SECRETORY SIGNAL RECOGNITION PARTICLE ASSEMBLY OF A 14-KDA SUBUNIT
OF 200 KDA SUBUNIT AND SIX PROTEIN SUBUNITS: SRP2, SRP3, SRP4,
SRP9, SRP14 AND SRP9.
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY BELONGS TO THE SRP14 FAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Institute
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. SRP9 by and for commercial
entities requires a license agreement (see <http://www.ict.bzh.ch/>)
or send an email to license@embl.ch)

EMBL	U57440	AAB02232.1	-
EMBL	M29265	AAA20988.1	-
PIR	A34501	A34501	-
DR	HSSP	P16354	1914
InterPro	IPR003210	SP14	-
Plan	P00290	SP14.1	-
Signal	Recognition	particle	RNA-binding
Conflict	2	2	2
SEQUENCE	110 AA	12487 MW	CD0106, IPR003210, SP14.1

Query Match	Score	DB	Length
62.2%	Score 57	DB 1	Length 111

functions as long as this document is in no way
at the not removed. (See http://www.ncbi.nlm.nih.gov/seq/seqsub-sib.ch)

functions as long as this document is in no way
at the not removed. (See http://www.ncbi.nlm.nih.gov/seq/seqsub-sib.ch)

functions as long as this document is in no way
at the not removed. (See http://www.ncbi.nlm.nih.gov/seq/seqsub-sib.ch)

AC Q45194;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DP Hypothetical A1 protein.
 GN W09G12.7.
 OG Caenorhabditis elegans
 OC Eukaryota, Metazoa, Nematozoa, Chordata, Phlebotomidae
 CC Phlebotomidae, Phlebotominae, Caenorhabditis
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RY VERIFIED against F.A.M.I. barrier;
 RA None;
 RT Genomic sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Genotyping Consortium;
 RL Science 282 2012-2018 (1998)
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RY Direct Submission;
 RA Submitted (FEB-1998) to the EMBL/GenBank/CCDB databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RT Direct Submission;
 RL Submitted (AUG-2001) to the EMBL/GenBank/CCDB databases.
 DP EMBL; AF047663; AAC04447 1;
 KW Hypothetical protein
 SC TrEMBLrel. 06 AA, 418.5 WW, AB443458-459-461A-46C64,
 46D; Match: 73.3%, 41.5%, 15.5%, length 324,
 Best Local Similarity 73.3%; Pred. No. 3.5;
 Matches 11, Conservative 0, Miscellaneous 4, Indels 0, Gaps 0;
 CY 1 DQFFFFFVCPFFV 10
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 DB 124 DQFFFFFVCPFFV 124

RESULT 3
 Q17336 PRELIMINARY; PRT; 897 AA.
 AC Q17336;
 DT 01-NOV-1998 (TrEMBLrel. 01, Created)
 DT 01-NOV-1998 (TrEMBLrel. 01, Last sequence update)
 DE LRT-458
 DE LRT-458
 OS Caenorhabditis elegans
 CC Eukaryota, Metazoa, Nematozoa, Chordata, Phlebotomidae
 CC Phlebotomidae, Phlebotominae, Caenorhabditis
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=L2;
 RA Kelly W.G., Coles L.H., Fire A.Z.,
 RL Genetics 0:0-0:06
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Matthews L.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/CCDB databases.
 DP EMBL; U19615; AA851351 1;
 DP EMBL; Z41723; AA854252 1;
 DP InterPro: IPR003891; IPR0140
 DR InterPro: IPR003891; IPR0140
 DR Pfam: PF02847; MA3.1
 DR Pfam: PF02854; MIF4G.1
 DP SMART; SM00544; MA3.1
 DP SMART; SM00543; MIF4G.1

SU SEQUENCE 897 AA; 104268 MW; AAB08445/AF0434 CRC64;
 Query Match 62.8%, Score 11, 18.1, length 327;
 Best Local Similarity 62.8%; Pred. No. 7.6;
 Matches 10, Conservative 0, Miscellaneous 0, Indels 0, Gaps 0;
 CY 3 DQFFFFFVCPFFV 16
 || ||||| ||
 DB 736 DQFFFFFVCPFFV 740

RESULT 4
 Q41111
 AC Q41111;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Dehydrin.
 OS Phaseolus vulgaris (Kidney bean) (French bean)
 CC Eukaryota, Viridiplantae, Streptophyta, Erythophyta, Tracheophyta,
 CC Spermatophyta, Magnoliopsida, Eufiditales, Euphorbiales, Euphorbiaceae,
 CC Euphorbiales, Euphorbiaceae, Euphorbiales, Euphorbiaceae, Euphorbiaceae,
 CC NCBI_TaxID=3895;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, SAXA;
 RA Chai T.Y., Purvard G.;
 RL Submitted (APR-1996) to the EMBL/GenBank/CCDB databases.
 DP EMBL; U54703; AA005541 1;
 DP InterPro: IPR00167; dehydrin.
 DP Pfam: PF00257; dehydrin; 1.
 DP FASIT; IPR00167; dehydrin; 1.
 DR PROSITE; PS00923; DEHYDRIN2; 2
 SC SEQUENCE 332 AA, 42933 WW, EMBLrel. 01-24-96 DEHYDRIN2;
 24-96; Match: 62.5%, 41.3%, 15.5%, length 102,
 Best Local Similarity 62.5%; Pred. No. 3;
 Matches 10, Conservative 0, Miscellaneous 0, Indels 0, Gaps 0;
 CY 1 DQFFFFFVCPFFV 16
 || ||||| ||
 DB 87 DQFFFFFVCPFFV 102

RESULT 5
 Q9H4J8
 ID Q9H4J8 PRELIMINARY; PRT; 315 AA.
 AC Q9H4J8;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE P1107011 (Unrel. HM) (High mobility group box protein) (fragment)
 DE P1107011 (Unrel. HM) (High mobility group box protein) (fragment)
 RN Homo sapiens (Human)
 CC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
 CC Mammalia, Eutheria, Primates, Catarrhini, Hominoidea, Homo,
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Clark G.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/CCDB databases.
 DP EMBL; AL014419; CAB91660 1;
 DP EMBL; U07155; HMV.
 DR InterPro: IPR000138; Highmobility_12.
 DR InterPro: IPR000138; Highmobility_12.
 DR InterPro: IPR000138; Highmobility_12.
 DR Pfam: PF00505; HMG box; 1.
 DR Pfam: PF00505; HMG box; 1.
 DR PRINTS; PR01217; PRICHTEXTEN.
 DR SMART; SM00328; HMG; 1.
 FT NON_TER 1

RESULT 14
Q8T1Y5 PRELIMINARY; PRT: 2254 AA.
AC Q8T1Y5; (TEMBRel: 21, Created
DT 01-JUN-2002 (TEMBRel: 21, Last sequence update)
DT 01-JUN-2002 (TEMBRel: 21, Last annotation update)
DE IRE (root hair elongation).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelidia; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Gleckner G., Eichinger L., Szafranski K., Pachter J., Dear P.,
EA Lehman G., Baumgart C., Paria J., April J.P., Guigo R., Humphreys A.,
EA Tussgaai E., Cox E., Quail M.A., Platzer M., Rosenthal A., Norder A.A.,
PT "Sequence and Analysis of Chromosome 2 of Dictyostelium."
RL Submitted (MAP-2002) to the EMBL/GenBank/DBJ databases
DR EMBL; AC116032; AAL93029.1;
SQ SEQUENCE 2254 AA; 251791 MW; 89281615CCE5624 (P7044);
Query March 50.1%; Score 49.5; DB 5; Length 2254;
Best Local Similarity 91.3%; Pred. No. 34;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 PFFFFFSPKSKS 14
EQ 033 PFFFFFSPKSKS 944
RESULT 15
Q8T9W5 PRELIMINARY; PRT: 1407 AA.
AC Q8T9W5;
DT 01-JUN-2002 (TEMBRel: 21, Created)
DT 01-JUN-2002 (TEMBRel: 21, Last sequence update)
DE ABC transporter ABCB2.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelidia; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Anjard C., Lomakin W.F.;
PT "Evolution of the ABC Transporters of Dictyostelium."
RL Submitted (CAN 2000) to the EMBL/GenBank/DBJ databases
DR EMBL; AF466305; AAL74249.1;
SQ SEQUENCE 1407 AA; 154763 MW; 81E6E5EEBA311DAR (P7044);
Query March 50.1%; Score 49.5; DB 5; Length 1407;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 12; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
QY 1 DCPFFFFVSPKSKS 16
EQ 727 DCPFFFFVSPKSKS 741
Search completed: March 3, 2003, 06:14:50
Job time : 35.7317 secs

13, treated)
13, last sequence update
13, last annotation update
PRT: 2009 AA.
AC 2009 AA;
DT 01-JUN-2002 (TEMBRel: 21, Created)
DT 01-JUN-2002 (TEMBRel: 21, Last sequence update)
DE IRE (root hair elongation).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelidia; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Gleckner G., Eichinger L., Szafranski K., Pachter J., Dear P.,
EA Lehman G., Baumgart C., Paria J., April J.P., Guigo R., Humphreys A.,
EA Tussgaai E., Cox E., Quail M.A., Platzer M., Rosenthal A., Norder A.A.,
PT "Sequence and Analysis of Chromosome 2 of Dictyostelium."
RL Submitted (MAP-2002) to the EMBL/GenBank/DBJ databases
DR EMBL; AC116032; AAL93029.1;
SQ SEQUENCE 2254 AA; 251791 MW; 89281615CCE5624 (P7044);
Query March 50.1%; Score 49.5; DB 5; Length 2254;
Best Local Similarity 91.3%; Pred. No. 34;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 PFFFFFSPKSKS 14
EQ 033 PFFFFFSPKSKS 944
RESULT 15
Q8T9W5 PRELIMINARY; PRT: 1407 AA.
AC Q8T9W5;
DT 01-JUN-2002 (TEMBRel: 21, Created)
DT 01-JUN-2002 (TEMBRel: 21, Last sequence update)
DE ABC transporter ABCB2.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelidia; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Anjard C., Lomakin W.F.;
PT "Evolution of the ABC Transporters of Dictyostelium."
RL Submitted (CAN 2000) to the EMBL/GenBank/DBJ databases
DR EMBL; AF466305; AAL74249.1;
SQ SEQUENCE 1407 AA; 154763 MW; 81E6E5EEBA311DAR (P7044);
Query March 50.1%; Score 49.5; DB 5; Length 1407;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 12; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
QY 1 DCPFFFFVSPKSKS 16
EQ 727 DCPFFFFVSPKSKS 741
Search completed: March 3, 2003, 06:14:50
Job time : 35.7317 secs

13, treated)
13, last sequence update
13, last annotation update
PRT: 2009 AA.
AC 2009 AA;
DT 01-JUN-2002 (TEMBRel: 21, Created)
DT 01-JUN-2002 (TEMBRel: 21, Last sequence update)
DE IRE (root hair elongation).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelidia; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Gleckner G., Eichinger L., Szafranski K., Pachter J., Dear P.,
EA Lehman G., Baumgart C., Paria J., April J.P., Guigo R., Humphreys A.,
EA Tussgaai E., Cox E., Quail M.A., Platzer M., Rosenthal A., Norder A.A.,
PT "Sequence and Analysis of Chromosome 2 of Dictyostelium."
RL Submitted (MAP-2002) to the EMBL/GenBank/DBJ databases
DR EMBL; AC116032; AAL93029.1;
SQ SEQUENCE 2254 AA; 251791 MW; 89281615CCE5624 (P7044);
Query March 50.1%; Score 49.5; DB 5; Length 2254;
Best Local Similarity 91.3%; Pred. No. 34;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 PFFFFFSPKSKS 14
EQ 033 PFFFFFSPKSKS 944
RESULT 15
Q8T9W5 PRELIMINARY; PRT: 1407 AA.
AC Q8T9W5;
DT 01-JUN-2002 (TEMBRel: 21, Created)
DT 01-JUN-2002 (TEMBRel: 21, Last sequence update)
DE ABC transporter ABCB2.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelidia; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Anjard C., Lomakin W.F.;
PT "Evolution of the ABC Transporters of Dictyostelium."
RL Submitted (CAN 2000) to the EMBL/GenBank/DBJ databases
DR EMBL; AF466305; AAL74249.1;
SQ SEQUENCE 1407 AA; 154763 MW; 81E6E5EEBA311DAR (P7044);
Query March 50.1%; Score 49.5; DB 5; Length 1407;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 12; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
QY 1 DCPFFFFVSPKSKS 16
EQ 727 DCPFFFFVSPKSKS 741
Search completed: March 3, 2003, 06:14:50
Job time : 35.7317 secs

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XX Claim 11, Page 70, 75pp, English.

XX The present peptide sequence represents a specifically claimed membrane

XX binding element. The invention relates to a soluble heterologous (A) of a

XX soluble polypeptide (B), which comprises at least 2 heterologous

XX membrane binding elements (MBE) of low molecular affinity, covalently

XX associated with (C). MBE interact, independently and with thermodynamic

XX affinity, with components of cellular or artificial membranes exposed

XX to extracellular fluids (A) are used to treat disorders treatable with

XX (i) itself, specifically inflammation or any other complement-related

XX disorder (e.g. neurological disease, graft rejection, myocardial

XX infarction, sepsis, rheumatoid arthritis and many others; including

XX allergic reactions, swelling, fever, fever, ischaemic stroke and as

XX immunomodulators for treating multiple sclerosis (A) are administered

XX orally, typically, by injection or inhalation at 0.01 to 10 (preferably

XX 0.1-10) mg/kg/day

XX Sequence 16 AA;

XX Query March 100 00, Score 92, PR 19, Length 16;

XX Best Local Similarity 100 00, Pred No 1 10000;

XX Matches 16, Conservative 0, Mismatches 0, Indels 0, Gaps 0.

QY 1 DDPKFFKFFKSPSSK 16

DB 1 DDPKFFKFFKSPSSK 16

RESULT 2

AAV59858

IE AAV59858 standard, Peptide, 16 AA.

XX AAV59858;

AC 1 DDPKFFKFFKSPSSK 16

DT 08-MAY-2000 (first entry)

XX Membrane binding element used in anti angiogenic polypeptide.

DE Anti angiogenic, angiogenesis inhibitor, membrane binding element,

XX cancer; tumour; therapy.

KW Synthetic.

OS WO2000094052 A2.

PN 27-JAN-2000.

XX 16-MAY-1999; 96W05060220

XX 16-MAY-1999; 96P 001-805

XX (ADFF-) ADFFOTECH PLC.

XX Smith RAG, Wright CF, Steward M, Cox VE;

XX wpl; 2000 182405/16.

XX New table below of anti angiogenic polypeptide useful for

XX treatment of primary or secondary cancers, contains covalently associated

XX membrane-binding elements for targeting

XX Claim 12, Page 32, 35pp, English.

XX The present sequence is a claim for a polypeptide-peptide

XX soluble binding element (MBE) that can be utilized in novel

XX soluble derivatives of anti-angiogenic polypeptides of the

XX invention. The peptide is a membrane binding MBE with low

XX molecular affinity that is covalently associated with a solid

XX anti-angiogenic polypeptide, such as a heterocyclic region of a

XX plasminogen, fragments of related proteins containing kringle

XX domains, fragments of collagen or fibrin, or fibrinogen.

CC antibodies against receptors for angiogenic mediators, and

CC anti-angiogenic factors, are used to treat angiogenesis, the

CC interact independently with thermodynamic affinity, with

CC components of the vascular endothelium (A) provide targeted

CC delivery of the anti-angiogenic polypeptide to cell membranes and

CC sites of active angiogenesis, particularly the vascular endothelium,

CC and thereby to inhibit the local concentration and reduce the

CC of adverse effects on normal tissues elsewhere in the vasculature.

CC They are used in a claimed method of treatment of primary or

CC secondary tumour.

XX Sequence 16 AA;

XX Query March 100 00, Score 92, PR 19, Length 16;

XX Best Local Similarity 100 00, Pred No 1 10000;

XX Matches 16, Conservative 0, Mismatches 0, Indels 0, Gaps 0.

QY 1 DDPKFFKFFKSPSSK 16

DB 1 DDPKFFKFFKSPSSK 16

RESULT 3

ABR61240

ID ABR61240 standard; peptide; 16 AA.

XX ABR61240;

XX 20-AUG-2002 (first entry)

XX Antibacterial membrane binding peptide SEQ ID NO.7.

XX Antibacterial, glycopeptide, Peptide membrane associating element;

XX bacterial infection; vancomycin, peptidoglycan biosynthesis inhibition;

XX antibiotic.

XX Synthetic.

XX WO2000016612-A1.

XX 10-MAY-2002.

XX 02-NOV-2001; 2001W03064467.

XX 03-NOV-2000; 2000P 00664024.

XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX (ADFF-) ADFFOTECH LTD.

XX Cooper MA, Reddy JR;

XX wpl; 2000 414492/50.

XX Antibacterial compound, useful for the treatment of a bacterial

XX infection by a 3 gram positive or negative bacterium, comprises a

XX conjugate of glycopeptide and peptide membrane associating element

XX Claim 1; Page 57; 64pp; English.

XX The present invention describes an antibacterial compound, comprising

XX a conjugate of glycopeptide and peptide membrane associating elements.

XX (i) comprises the formula V (X), where V is a glycopeptide moiety that

XX inhibits peptidoglycan biosynthesis in bacteria; X is a living group;

XX is a peptide membrane associating element; and X is H or a membrane

XX associating element. Also described is a method of treating or preventing

XX a bacterial infection, comprising the administration of (i) and (ii) to

XX of (i) in the manufacture of a solid support for the treatment or prevention

XX of a bacterial infection. (ii) are used in the manufacture of a medicament

XX for the treatment or prophylaxis of a bacterial infection in a patient

XX animal to be, including both the gram positive and gram negative bacteria

XX including *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus*

XX *epidermidis* sp., *Vibrio* sp., *Helicobacter* sp., *Parityella* sp., *Streptococcus* sp.,

Query Match 100.00; Score 82; DB 21; Length 17;
 Best Local Similarity 100.00; Pred. NO. 9e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PDPKPKPKPKPKPKPKSK 15
 |||||
 DB 2 PDPKPKPKPKPKPKSK 17

RESULT 6

AAW45878
 ID AAW45878 standard; peptide; 16 AA.

XX AAW45878;

XX 30-JUN-1998 (first entry)

XX Peptide membrane binding element.

XX Membrane binding element; thrombotic disease; inflammation;
 complement related disease; soluble peptide

XX Synthetic

XX W09RC2474-A2

XX 22 JAN 1998.

XX 08 JUL 1997; 09WO EP07376

XX 15 JUL 1996; 96CP-0014871.

XX (ADPR-) ADPRTECH PLC.

XX Dodd I, Mossakowska DFL, Smith PAG;

XX WFI, 1998 1102347/0

XX Derivatives of soluble fully peptide(s) bound to low affinity
 membrane binding groups useful for treating complement-related and
 thrombotic diseases, providing improved localisation at cellular
 membranes

XX Claim 11; Page 70; 75pp; English.

XX The present peptide sequence represents a specifically defined membrane
 binding element. The invention relates to a soluble derivative (A) of a
 soluble polypeptide (1), which comprises at least 2 heterologous
 membrane-binding elements (MBEs) of low membrane affinity associated
 associated with (1). MBE interact, independently and with thermodynamic
 activity, with components of cellular or artificial membrane exposed
 to extracellular fluids. (A) are used to treat disorders treatable with
 (1) itself, specifically inflammation or any other complement-related
 disorder, e.g. neurological disease, graft rejection, myocardial
 infarction, sepsis, rheumatoid arthritis and many others; including
 application to indwelling devices) and thrombotic disease, but also to
 treat allergy, induce weight loss, to treat ischemia or asthma and as
 immunomodulators for treating multiple sclerosis (A) are administered
 orally, intrally, by injection or inhalation at 0.01-10 (preferably
 0.1-10) mg/kg/day

XX Sequence 16 AA;

Query Match 93.00; Score 77; DB 19; Length 16;
 Best Local Similarity 100.00; Pred. NO. 9e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PDPKPKPKPKPKPKSK 15
 |||||
 DB 1 PDPKPKPKPKPKPKSK 15

RESULT 7

AAV58855

XX AAV58855 standard; Peptide; 16 AA.

XX AAV58855;

XX 08-MAY-2000 (first entry)

XX Membrane binding element used in anti-angiogenic polypeptide.

XX Anti-angiogenic; angiogenesis inhibitor; membrane binding element;
 cancer; tumour; therapy.

XX Synthetic.

XX W0200004052-A2.

XX 27-JAN-2000.

XX 16 JUL 1999; 99WO GB02292.

XX 16-JUL-1999; 99CP-0014505.

XX (ADPR-) ADPRTECH PLC.

XX Smith PAC, Bright JR, Steward M, Cox VF;

XX WFI, 2000 102406/16.

XX A low soluble derivative of anti-angiogenic polypeptide useful for
 treatment of primary or secondary cancers, contains covalently attached
 membrane-binding elements for targeting

XX Claim 14; Page 34; 35pp; English.

XX The present sequence is a claimed example of a lysine-rich peptide
 membrane binding element (MBE) that can be utilised in novel
 soluble derivatives (A) of anti-angiogenic polypeptides of the
 invention. (A) comprise 2 or more heterologous MBEs with low
 membrane affinity that are covalently attached to a soluble
 anti-angiogenic polypeptide (1) and a third region of human
 plasmaogen, fragments of related proteins containing kringle
 domains, fragments of collagen or prolactin, neutralising
 antibodies against receptors for angiogenic mediators, and
 antagonists of integrins involved in angiogenesis. The MBEs
 interact independently with thermodynamic activity, with
 components of the vascular endothelium, fibroblasts, myocytes
 delivery of the anti-angiogenic polypeptide to cell membranes and
 sites of active angiogenesis, particularly the vascular endothelium,
 and therefore increase the local concentration and efficacy of the
 of adverse effects on normal processes elsewhere in the vasculature.
 They are used in a clinical trial for treatment of primary or
 secondary tumour.

XX Sequence 16 AA;

Query Match 93.00; Score 77; DB 21; Length 16;
 Best Local Similarity 100.00; Pred. NO. 9e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PDPKPKPKPKPKPKSK 15
 |||||
 DB 1 PDPKPKPKPKPKPKSK 15

RESULT 8

ABB81237

XX ABB81237 standard; peptide; 16 AA.

XX ABB81237;

XX 20-AUG-2002 (first entry)

FT Modified-site 1 /note= "myristoylated"
 FT
 PN WO200004052 A2.
 XX 27 JAN 2000.
 XX
 XX 16-JUL-1999; 99WO 3802202.
 PF
 XX 16-JUL-1998; 98GB-0015505.
 PR
 XX (ADPR-) ADPROTECH PLC.
 PA
 XX Smith PAC, Bright AP, Steward M, Cox VP;
 PI
 XX WPI; 2000 192406/16.
 DR
 XX
 XX New soluble derivative of anti-angiogenic polypeptide useful for
 PT treatment of primary and secondary cancers, contains covalently attached
 FT membrane-binding elements for targeting
 XX
 XX Disclosure, Page 13; 36pp; English.
 XX
 CC The present sequence is an example of a lysine rich peptide
 CC membrane binding element (MBE) that can be utilised in novel
 CC soluble derivatives (1) of anti-angiogenic polypeptides of the
 CC invention. (iv) comprise 2 or more heterologous MBEs with low
 CC membrane affinity that are covalently attached to a soluble
 CC anti-angiogenic polypeptide such as a non-catalytic region of human
 CC plasminogen, fragments of related proteins containing fibrin-
 CC domains, fragments of collagen or fibronectin, neurotising
 CC antibodies against receptors for angiogenic mediators, and
 CC arrays of integrins involved in angiogenesis. The MBEs
 CC interact independently with thermodynamic affinity, with
 CC components of the vascular endothelium. (ii) provide targeted
 CC delivery of the anti-angiogenic polypeptide to cell membranes and
 CC sites of active angiogenesis, particularly the vascular endothelium,
 CC and therefore increase the local concentration and reduce the risk
 CC of adverse effects on normal processes elsewhere in the vasculature.
 CC They are used in a claimed method of treatment of primary or
 CC secondary tumour.
 XX
 XX
 SQ Sequence 17 AA;
 Query Match 91.0%, Score 77, DR 21; Length 88;
 Best Local Similarity 100.0%, Pred No. 0.00045;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Caps 0;
 QY 1 DGPFFFFFFSPSS 15
 DB 1 DGPFFFFFFSPSS 15
 RESULT 11
 ABB07540
 ID ABB07540 standard; peptide: 98 AA.
 XX
 AC ABB07540;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Amino acid sequence of APT2065.
 XX
 CC cccc, lipid raft, derivative, DAF, non-epitope, non-topical; human;
 PW cerebroprotective; anti-epileptic; anti-allergic; antitubercular; cardiac;
 PW antiparasitic; antitubercular; dermatological; hypertensive; vasodilator;
 PW antileishmanial; anti-influenza; anti-inflammatory; antihistaminic;
 PW immunosuppressive; antianemic; nephrotropic; antileishmanial;
 KW antitubercular; antitubercular; anti-viral;
 XX
 CC Synthesis
 CC Homo sapiens

FH Key Location/Qualifiers
 FT Disulfide bond 71-72 "disulfide bridge"
 FT
 XX WO200004638 A1.
 PW
 XX 17-JAN-2002.
 XX
 XX 06-JUL-2001; 2001WO-0800034.
 PF
 XX 07-JUL-2000; 2000GB-0016811.
 PR
 XX (ADPR-) ADPROTECH LTD.
 PA
 XX Rowling RUE, Smith GP, Ridley SH;
 PI
 XX WPI; 2000 164646/21
 DR
 XX
 XX Lipid raft, derivative of a soluble polypeptide, a soluble
 FT complement regulatory molecule for treating disorders involving
 FT complement activity and various inflammatory, neurological and immune
 FT disorders
 XX
 XX Example 5; Page 47; Sipp; English.
 XX
 CC The invention relates to a soluble derivative (1) of a soluble
 CC polypeptide (2) having at least two heterologous membrane binding elements
 CC with low membrane affinity covalently attached to the polypeptide,
 CC the elements being capable of interacting with components of cellular or
 CC artificial membranes exposed to extracellular fluids and target lipid
 CC raft components of membrane. (ii) is useful for treating disorders
 CC amenable to treatment by a soluble peptide fragment of (2)(3), DAF or other
 CC therapeutic agent, and for the preparation of a medicament for treatment
 CC of disorders involving complement activity and various inflammatory and
 CC immune disorders. (iv) is useful for treating neurological disorders (e.g.
 CC multiple sclerosis, stroke, Parkinson's, Alzheimer's disease, traumatic
 CC brain injury and allergic encephalitis), disorders of inappropriate or
 CC undesirable complement activation (e.g. xenograft rejection, cortical
 CC graft rejection), inflammatory disorders (including rheumatoid arthritis,
 CC Crohn's disease, uveitis, psoriasis, asthma, scleroderma, acute
 CC pancreatitis, post-ischemic reperfusion syndrome, angiodermatitis,
 CC infarction, hypertension, renal ischaemia, testicular atrophy, atherosclerosis),
 CC infectious diseases or sepsis (e.g. multiple organ failure, septic
 CC shock), autoimmune diseases (e.g. rheumatoid arthritis, systemic lupus
 CC erythematosus, haemolytic anaemia, glomerulonephritis and vasculitis)
 CC diagnosis of, detection of, disorders (e.g. infertility, complement mediated
 CC infertility), and wound healing. The present sequence represents the
 CC amino acid sequence of APT2065.
 XX
 XX
 SQ Sequence 88 AA;
 Query Match 91.0%, Score 77, DR 21; Length 88;
 Best Local Similarity 100.0%, Pred No. 0.00045;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Caps 0;
 QY 1 DGPFFFFFFSPSS 15
 DB 73 DGPFFFFFFSPSS 87
 RESULT 12
 ABB07538
 ID ABB07538 standard; peptide: 99 AA.
 XX
 AC ABB07538;
 XX
 XX 23-APR-2002 (first entry)
 XX
 DE Amino acid sequence of APT2065.
 XX
 CC cccc, lipid raft, derivative, DAF, non-epitope, non-topical; human;
 PW cerebroprotective; anti-epileptic; anti-allergic; antitubercular; cardiac;
 PW antiparasitic; antitubercular; dermatological; hypertensive; vasodilator;
 PW immunosuppressive; antianemic; nephrotropic; antileishmanial;
 KW antitubercular; antitubercular; anti-viral;
 XX
 CC Synthesis
 CC Homo sapiens

RESULT 14

AAW45898
 ID AAW45898 standard; peptide; 214 AA.
 XX
 AC AAW45898;
 DT 30-JUN-1999 (first entry)
 XX
 DE SCP 1-3 of complement receptor type 1 (CR1)/switch fusion protein.
 XX
 KW Membrane binding element, thrombotic disease, soluble protein,
 KW complement-related disease, integral membrane protein, inflammation,
 KW short consensus repeat, SCRP 1, C3b, complement receptor type 1
 XX
 CC Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Cross-links 214
 FT /note= "Disulphide linked to Cys in peptide given
 FT in AAW45898 or 2 (HLK)200H(CHL)120H3".
 PN W09AC2454 A2.
 XX 22 JAN-1999.
 XX
 XX 08-JUL-1997; 97WO-EP03715.
 XX
 XX 15-JUL-1996; 96GB-0014871.
 PR
 PA (ADPR-) ADPROTECH PLC.
 XX
 PI Dodd I, Mossakowska DEI, Smith PAG;
 XX WPI; 1998-110524/10.
 DR
 XX
 XX Derivatives of soluble glycopeptide(s) bonded to low affinity
 PT membrane binding groups - useful for treating complement-related and
 PT thrombotic diseases, providing improved localisation at cellular
 PT membranes
 XX
 PS Claim 22, Page 60, figg, English
 XX
 CC This sequence represents a specifically claimed protein having the
 CC amino acid sequence of short consensus repeats (SCR 1-3) of
 CC complement receptor type (CRP) plus a switch fusion sequence. The
 CC invention relates to a soluble derivative (A) of a soluble polypeptide
 CC (1), which comprises at least 2 heterologous membrane-binding elements
 CC (MRB) of low membrane affinity covalently associated with (i) MBP
 CC interact, independently and with thermodynamic additivity, with
 CC components of cellular or artificial membranes exposed to extracellular
 CC fluids. (A) are used to treat disorders treatable with (i) itself,
 CC (ii) immunological disease, graft rejection, myocardial infarction,
 CC sepsis, rheumatoid arthritis and many others; including application to
 CC indwelling devices) and thrombotic disease, but also to treat allergy,
 CC induce weight loss, to treat ischaemia or asthma and as immun-
 CC modulators for treating multiple sclerosis. (A) are administered orally,
 CC topically, by injection or inhalation or as a gel (preferably as a
 CC hydrogel).
 XX
 SQ Sequence 214 AA;
 Query March 03 08; Query 75, 78 101; length 214.
 Best local similarity: 100.00, E-Val 0.000000
 Matches: 16, Conservation: 3, Mismatches: 6, Indels: 0, Gaps: 0,
 QY 1 DQFFFFFVFSTFSS 15
 DB 198 DGPFFFFKSPSSPS 212

RESULT 15

AAW75987
 ID AAW75987 standard; Protein; 215 AA.
 XX
 AC AAW75987;
 DT 18-JAN-1999 (first entry)
 XX
 DE Complement receptor type 1-like polypeptide PM-9.
 XX
 KW Complement receptor type-1; C3b, C3b, PM-9, complement, inhibitor;
 KW myristoyl/electrostatic switch peptide reagent 1; MSWP-1;
 KW anti-phagocytosis; multiple sclerosis; Parkinson's disease;
 KW xenograft rejection, inflammation, Crohn's disease, asthma;
 KW paracetamol; first ischaemic reperfusion, infection, sepsis;
 KW autoimmune disease; rheumatoid arthritis; proliferative nephritis;
 KW myasthenia gravis; reproductive disorder; therapy.
 XX
 OS Chimeric - Homo sapiens.
 OS Chimeric - Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..197
 FT /label= CW7
 FT Peptide 199..215
 FT /label= MSWP-1
 FT Disulfide-bond 198..199
 FT Modified-site /note= "(S-2 thiopyridyl)cysteine"
 FT Modified-site 215 /note= "N (myristoyl) Glycine"
 FT
 XX W09839433-A1.
 PN
 XX 11-SEP-1998.
 PD
 XX 05-MAR-1998; 98WO-GB00727.
 PF
 XX 05-MAR-1997; 97GB 000419.
 PF
 XX (ADPR-) ADPROTECH PLC.
 PA
 XX Cox VP, Mossakowska DEI, Smith PAG;
 PI Cox VP, Mossakowska DEI, Smith PAG;
 XX WPI; 1998-00004/43.
 XX
 XX Soluble polypeptide comprising short consensus repeats from LRR-A
 PT used to treat disorders and diseases associated with inflammation or
 PT inappropriate complement activation
 XX
 XX Claim 17, Page 50-52, 67ff, English.
 XX
 CC This is the amino acid sequence of PM 1, or (C3b) Cys 3-5 (MSWP-1),
 CC comprising novel soluble complement receptor type 1 (C3b) like
 CC polypeptide (A) (see AAW75987) joined to a myristoyl/electrostatic
 CC switch peptide reagent 1 (MSWP-1). It was prepared by coupling
 CC CMT/Cys (see AAW75987) to a synthetic MSWP-1 peptide. CMT comprises
 CC the short consensus repeats (SCR) 1 and 2 from C3b and SCR of the
 CC C3b-like protein (see AAW75987). Soluble C3b derived proteins of the
 CC invention (see AAW75987-47 and AAW75987-48) are complement inhibitors
 CC with functional complement inhibitory, including anti-biolytic,
 CC activity. These can be used to treat a disease or disorder
 CC associated with inflammation or inappropriate complement activation,
 CC such as neurological disorders (eg, multiple sclerosis, Parkinson's
 CC disease), disorders of inflammation or defective complement
 CC activation (eg, xenograft rejection, inflammatory disorders (e.g.
 CC Crohn's disease, asthma), and acute pulmonary infection, post-ischaemic
 CC reperfusion syndromes, infection, sepsis, myocardial infarction,
 CC rheumatoid arthritis and many others; including application to
 CC indwelling devices and thrombotic disease, and also to treat allergy,
 CC proliferative nephritis and myasthenia gravis), and reproductive
 CC disorders
 XX
 SQ Sequence 215 AA;

4; Score 77; IP 14; Length 215;
20; Pred.No. 211;
; Mismatches 0; Indels 0; Gaps 0;

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software version 3.1.1
10/11/2003 - 2003 completed

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1, 1014:53 / Search time 10144 Seconds
(without alignment)
12,416,411,113 well updates/sec

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SEARCH 10

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1014:26 residues

int-bases parameters: 1014:566

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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (100)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (129)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (147)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-214-913-40

Query Match 56.11; Score 46; DB 10; Length 147;

Best Local Similarity 56.11; Field No. 11;

Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

CY 3 DPEYKPKPKPKPKPK 16

DB 125 DPEYKPKPKPKPKPK 140

RESULT 9

US-09-214-913-40

Sequence 1087, Application US/09090200

Patent No. US09090200A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA102

CURRENT APPLICATION NUMBER: US/09/090200

PRIOR FILING DATE: 2001-08-16

PRIOR APPLICATION NUMBER: PCT/US00/05883

PRIOR FILING DATE: 2000-04-08

PRIOR APPLICATION NUMBER: 60/124,270

NUMBER OF SEQ ID NOS: 1556

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1087

LENGTH: 154

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (40)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (42)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (60)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (83)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (94)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (85)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (96)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (100)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (113)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (115)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (122)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (124)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (129)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (132)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (146)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (147)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (149)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (153)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-214-913-40

Query Match

56.11; Score 46; DB 10; Length 154;

Best Local Similarity 56.11; Field No. 12;

Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CY 3 DPEYKPKPKPKPK 16

DB 8 DPEYKPKPKPKPK 21

RESULT 10

US-10-001-843-143

Sequence 143, Application US/10001843

Patent No. US0002013255A1

GENERAL INFORMATION:

APPLICANT: Salceda, Susana

APPLICANT: Macina, Roberto

APPLICANT: Pecipon, Hervé

APPLICANT: Cafferty, Robert

APPLICANT: Sun, Yongming

APPLICANT: Liu, Chenghua

APPLICANT: Turner, Leah

TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Cells and

FILE REFERENCE: PCT/US01/001,843

CURRENT APPLICATION NUMBER: US/10/001,843

PRIOR FILING DATE: 2001-11-30

PRIOR APPLICATION NUMBER: 60/240,993

PRIOR FILING DATE: 2000-11-20

NUMBER OF SEQ ID NOS: 218

SOFTWARE: PatentIn version 3.1

SEQ ID NO 143

LENGTH: 213

TYPE: PRT

ORGANISM: Homo sapien

US-10-001-843-143

Query Match 56.11; Score 46; DB 10; Length 213;

Best Local Similarity 56.11; Field No. 16;

Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CY 3 DPEYKPKPKPKPK 16

DB 180 DPEYKPKPKPKPK 202

RESULT 11

US-09-214-913-40


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? APPLICANT: Rosen et al.
? TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
? FILE REFERENCE: PA102
? CURRENT APPLICATION NUMBER: US/23/225,299
? PRIOR FILING DATE: 2001-08-10
? PRIOR APPLICATION NUMBER: PCT/US00/05aaa
? PRIOR FILING DATE: 2000-03-08
? PRIOR APPLICATION NUMBER: 50/124,270
? PRIOR FILING DATE: 1999-03-12
? NUMBER OF SEQ ID NOS: 1556
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 1408
? LENGTH: 36
? TYPE: PRT
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: SITE
? LOCATION: (4)
? OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
? NAME/KEY: SITE
? LOCATION: (6)
? OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
? NAME/KEY: SITE
? LOCATION: (8)
? OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
? NAME/KEY: SITE
? LOCATION: (12)
? OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
? NAME/KEY: SITE
? LOCATION: (13)
? OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
? NAME/KEY: SITE
? LOCATION: (36)
? OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1408

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Query Match      54.9%; Score 45; DB 10; Length 36;
Best local Similarity 60.9%, Pred. No. 3.9,
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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CY      2 GPRKFKKSPKSKK 16
      |||||
Db      20 GPRKFKKSKK 34

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Search completed: Mar 3, 2003, at 4:33
Job time : 48.0244 secs

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Source: The version 5.0 - 2003 release.

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Figure 1

[illegible]

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100-443887-1100

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 equal to the score of the result being printed,
 of the total score distribution.

SUMMARY

NO	DESCRIPTION
1	Sequence 78, April
2	Sequence 19, April
3	Sequence 20, April
4	Sequence 11, April
5	Sequence 11, April
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8	Sequence 31, April
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100	Sequence 5, April

Query Match 56.1%; Score 46; DB 4; Length 17;
Best Local Similarity 71.4%; Pred. No. 614;
Matches 10; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

DB 4 PPKPKPKPKPKPKPK 17

RESULT 2
US-08-462-096-11
Sequence 11, Application US/08/462,096B
Patent No. 6018030
GENERAL INFORMATION:
APPLICANT: Thatcher, David R.
APPLICANT: Wilks, Paula F.
TITLE OF INVENTION: Utilization of Gene Delivery and Gene Delivery System
FILE REFERENCE: CAC00026
CURRENT FILING DATE: 03/03/00
CURRENT FILING DATE: 03/03/00
EARLIER APPLICATION NUMBER: 08/000,000
EARLIER FILING DATE: 03/03/00
NUMBER OF SEQ. ID NOS: 25
SOFTWARE: Patent in Ver. 2.1
SEQ. ID NO. 10
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: UNUSUE
LOCATION: (30)
OTHER INFORMATION: Xaa is Cys with Acm sidechain
FEATURE:
OTHER INFORMATION: Identified as a Artificial Sequence: PPKPK

US-08-462-096-11

Query Match 56.1%; Score 46; DB 4; Length 30;
Best Local Similarity 71.4%; Pred. No. 104;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

DB 4 PPKPKPKPKPKPKPK 16

RESULT 3
US-08-462-096-20
Sequence 20, Application US/08/462,096B
Patent No. 6018030
GENERAL INFORMATION:
APPLICANT: Ferrari, Franco A.
APPLICANT: Richardson, Charles
APPLICANT: Chambers, James
APPLICANT: Gausey, Stuart
APPLICANT: Collier, Thomas A.
APPLICANT: Cappellio, Joseph
APPLICANT: Crissman, John W.
TITLE OF INVENTION: Peptides Containing Repetitive
NUMBER OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
NUMBER OF SEQUENCES: 112
CORRESPONDENCE ADDRESS:
ADDRESS: Fehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
C-MUTILES: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBERS: US/08/462,096B
FILING DATE: 07 JUN 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/462,096B
FILING DATE: 04 NOV 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/114,619
FILING DATE: 29 OCT 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/003,049
FILING DATE: 07 MAR 1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/175,155
FILING DATE: 23 DEC 1999
ATTORNEY/AGENT INFORMATION:
NAME: Treppert, Richard F.
REGISTRATION NUMBER: 31,801
FEDERAL REGISTER NUMBER: A 01249 P 01249
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-791-1000
TELEFAX: 415-385-7749
INFORMATION FOR SEQ. ID NO. 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQ. ID NO. 20

Query Match 56.1%; Score 46; DB 4; Length 295;
Best Local Similarity 90.9%; Pred. No. 12;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 4 PPKPKPKPKPKPKPK 14

RESULT 4
US-07-814-964-11
Sequence 11, Application US/07/814,964
Patent No. 5359047
GENERAL INFORMATION:
APPLICANT: Donahue, Brian A.
APPLICANT: Tacey, Jeffrey H.
APPLICANT: Bruhn, Suzanne L.
APPLICANT: Pili, Pieter M.
APPLICANT: Brown, Steven
APPLICANT: Kellett, Patti
APPLICANT: Essigmann, John M.
APPLICANT: Lippard, Stephen J.
TITLE OF INVENTION: DNA Structure Specific Recognition
NUMBER OF INVENTION: Protein and Gases Therefor
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESS: Hamilton, Frank, Smith & Reynolds, P.C.
STREET: 2000 Millbrae Drive
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90273

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
C-MUTILES: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/814,964
FILING DATE: 19911226
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

1 APPLICANT: Brown, Steven
2 APPLICANT: Kellett, Patti
3 TITLE OF INVENTION: Uses For DNA Structure Specific
4 TITLE OF INVENTION: Recognition Proteins
5 NUMBER OF SEQUENCES: 8
6 CORRESPONDENCE ADDRESS:
7 ADDRESSEE: Patent Administration, Tessa, Rutwiler & Thibault
8 CITY: Boston
9 STATE: MA
10 COUNTRY: USA
11 ZIP: 02109
12 COMPUTER READABLE FORM
13 MEDIUM TYPE: Floppy disk
14 OPERATING SYSTEM: PC-DOS/MS-DOS
15 SOFTWARE: Patent Release #1.0, Version #1.25
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/08/125,409
18 FILING DATE:
19 CLASSIFICATION: 435
20 ATTORNEY/AGENT INFORMATION:
21 NAME: Fenton, Gillian M
22 REGISTRATION NUMBER: 36,509
23 REFERENCE NUMBER: MIT 477/24
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: 617-248-7000
26 TELEFAX: 617-248-7100
27 INFORMATION FOR SEQUENCE CHARACTERISTICS:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 723 amino acids
30 TYPE: amino acid
31 TOPOLOGY: linear
32 MOLECULE TYPE: protein
33 ORIGINAL SOURCE:
34 ORGANISM: Drosophila melanogaster
35 IMMEDIATE SOURCE:
36 CLONE: Drosophila SSCP (predicted)
37 FEATURE:
38 NAME/KEY: Domain
39 LOCATION: 458-507
40 OTHER INFORMATION: /label= Acidic
41 FEATURE:
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43 LOCATION: 518-547
44 OTHER INFORMATION: /label= Basic I
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46 NAME/KEY: Domain
47 LOCATION: 632-749
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49 FEATURE:
50 NAME/KEY: Domain
51 LOCATION: 657-723
52 OTHER INFORMATION: /label= Mixed Charge
53 OR 125409-5
54
55 Query Match 50.18, Date 05, 22 1, Length 723,
56 Best total Similarity 50.04, Pos. 23, 23,
57 No. 435 9, Conservative 1, Mismatch 6, Indel 0,
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1 APPLICANT: Donahue, Brian A.
2 APPLICANT: Toney, Jeffrey H.
3 APPLICANT: Fruhn, Suzanne L.
4 APPLICANT: Pili, Pieter M.
5 APPLICANT: Brown, Steven
6 APPLICANT: Kellett, Patti
7 APPLICANT: Fessigmann, John M.
8 APPLICANT: Lippard, Stephen J.
9 TITLE OF INVENTION: DNA Structure Specific Recognition
10 TITLE OF INVENTION: Protein and Uses Therefor
11 NUMBER OF SEQUENCES: 13
12 CORRESPONDENCE ADDRESS:
13 ADDRESSEE: Hamill PC, Brock, Smith & Reynolds, P.C.
14 STREET: 2 Militia Drive
15 CITY: Lexington
16 STATE: MA
17 COUNTRY: USA
18 ZIP: 01173
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: Floppy disk
21 OPERATING SYSTEM: IBM PC compatible
22 SOFTWARE: Patent Release #1.0, Version #1.25
23 CURRENT APPLICATION DATA:
24 APPLICATION NUMBER: MIT 477/24
25 FILING DATE: 19921218
26 CLASSIFICATION:
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: US 07/589,906
29 FILING DATE: 19 JUN 1990
30 ATTORNEY/AGENT INFORMATION:
31 NAME: Granahan, Patricia
32 REGISTRATION NUMBER: 33,337
33 REFERENCE/DOCKET NUMBER: MIT-4787AAA
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: 617-861-6240
36 TELEFAX: 617-861-9540
37 INFORMATION FOR SEQUENCE CHARACTERISTICS:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 723 amino acids
40 TYPE: AMINO ACID
41 TOPOLOGY: linear
42 MOLECULE TYPE: protein
43 ORIGINAL SOURCE:
44 ORGANISM: Drosophila melanogaster
45 IMMEDIATE SOURCE:
46 CLONE: Drosophila SSCP (predicted)
47 FEATURE:
48 NAME/KEY: Domain
49 LOCATION: 458-507
50 OTHER INFORMATION: /label= Acidic
51 FEATURE:
52 NAME/KEY: Domain
53 LOCATION: 518-547
54 OTHER INFORMATION: /label= Basic I
55 FEATURE:
56 NAME/KEY: Domain
57 LOCATION: 547-620
58 OTHER INFORMATION: /label= Mixed Charge
59 FEATURE:
60 NAME/KEY: Domain
61 LOCATION: 657-723
62 OTHER INFORMATION: /label= Mixed Charge
63 PCT-US92-11107-11

Query Match 50.18, Score 46, DB 5, Length 723,
Best total Similarity 50.04, Pos. 23, 29,
Mismatch 9, Conservative 1, Mismatch 6, Indels 0,
Page 4

RESULT 10
PCT-US-94-04456-11
Sequence 5, Application US/09306044
GENERAL INFORMATION:
APPLICANT: GROCE, CARLO
APPLICANT: CANAANI, ERI
TITLE OF INVENTION: Diagnostic, Therapeutic and Methods
TITLE OF INVENTION: Detection and Treatment of Acute Leukemia
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the A11
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodstock, Washburn, Kurtz, Macklewitz &
ADDRESSEE: Norris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.02
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04496
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca Esq., Mark
REGISTRATION NUMBER: 33,229
REFERENCE/PATENT NUMBER: TSP 1242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568 3100
TELEFAX: (215) 568 3439
INFORMATION FOR SEQ ID NO. 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US-94-04456-11

Query Match 55.5%, Score 46.5, E-Value 1.0, Length 559,
Best Local Similarity 57.0%, Pct. No. 37,
Matches 11; Conservative 2, Mismatches 3, Indels 3, Gaps 1.

27 1 GATV PFFPKSPSPSSK 16
||| ||||| |||
Db 271 DEPPFAAPFPPSPSPSSK 300

RESULT 11
US-08-894-339-5
Sequence 5, Application US/09306044
Patent No. 5945400
GENERAL INFORMATION:
APPLICANT: SHERMAN, DANIEL
APPLICANT: RYK, GERARDO
APPLICANT: SCHWARTZ, BERTRAND
TITLE OF INVENTION: NUCLEIC ACID CONTAINING COMPOSITION,
PREPARATION AND USE THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pharm-Polysar, Peter, Inc.
STREET: 500 Arcola Road, Mailstop 3043
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,044
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/894,339
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP94/00048
FILING DATE: 15-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky Esq., Martin F.

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/894,339
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/00048
FILING DATE: 17-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP94/00048
FILING DATE: 15-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky Esq., Martin F.

Query Match 54.9%, Score 45, E-Value 1.7,
Best Local Similarity 57.0%, Pct. No. 11,
Matches 8; Conservative 2, Mismatches 4, Indels 0, Gaps 0.

27 3 PFFPKSPSPSSK 16
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21 2 DEPPFAAPFPPSPSPSSK 16

RESULT 12
US-09-306-044-5
Sequence 5, Application US/09306044
Patent No. 5945400
GENERAL INFORMATION:
APPLICANT: SHERMAN, DANIEL
APPLICANT: RYK, GERARDO
APPLICANT: SCHWARTZ, BERTRAND
TITLE OF INVENTION: NUCLEIC ACID CONTAINING COMPOSITION,
PREPARATION AND USE THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pharm-Polysar, Peter, Inc.
STREET: 500 Arcola Road, Mailstop 3043
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,044
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/894,339
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP94/00048
FILING DATE: 15-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky Esq., Martin F.

Best Local Similarity 57.1%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
CY 3 PPKYKPKSPKSK 16
DB 146 PPKSAKTPPKAK 159
||| ||| ||| |||
RESULT 14
US-08-837-058-1
; Sequence 1, Application US/08837058
; Patent No. 6074835
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan R.
; APPLICANT: Eggena, Mark
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
; TITLE OF INVENTION: Histone H1
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 200
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; CREATING SYSTEM: PC-DOSE/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,158
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-PW 2418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..212
; OTHER INFORMATION: /note="product - Human Histone
; OTHER INFORMATION: H1-S-1"
US-08-837-058-1
Query Match 54.9%; Score 45; DB 3; Length 212;
Best Local Similarity 57.1%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
CY 3 PPKYKPKSPKSK 16
DB 146 PPKSAKTPPKAK 159
||| ||| ||| |||
RESULT 15
US-09-041-889-4
; Sequence 4, Application US/09041889
; Patent No. 6033864
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; APPLICANT: Conavy, Ofer
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using

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US/09041889-4
PATENT NO. 6033864
APPLICANT: BRAUN, JONATHAN
APPLICANT: CONAVY, OFER
TITLE OF INVENTION: DIAGNOSIS, PREVENTION AND TREATMENT OF
TITLE OF INVENTION: ULCERATIVE COLITIS, AND CLINICAL SUBTYPES THEREOF, USING
TITLE OF INVENTION: HISTONE H1
BEST LOCAL SIMILARITY 57.1%; PRED. NO. 13;
MATCHES 8; CONSERVATIVE 2; MISMATCHES 4; INDELS 0; GAPS 0;
CY 3 PPKYKPKSPKSK 16
DB 146 PPKSAKTPPKAK 159
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RESULT 14
US-08-837-058-1
; Sequence 1, Application US/08837058
; Patent No. 6074835
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan R.
; APPLICANT: Eggena, Mark
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
; TITLE OF INVENTION: Histone H1
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 200
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; CREATING SYSTEM: PC-DOSE/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,158
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-PW 2418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..212
; OTHER INFORMATION: /note="product - Human Histone
; OTHER INFORMATION: H1-S-1"
US-08-837-058-1
Query Match 54.9%; Score 45; DB 3; Length 212;
Best Local Similarity 57.1%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
CY 3 PPKYKPKSPKSK 16
DB 146 PPKSAKTPPKAK 159
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RESULT 15
US-09-041-889-4
; Sequence 4, Application US/09041889
; Patent No. 6033864
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; APPLICANT: Conavy, Ofer
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using

```

1 TITLE OF INVENTION: Microbial UC PANCA antigens
2 NUMBER OF SEQUENCES: 41
3 CORRESPONDENCE ADDRESS:
4 ADDRESSEE: Campbell & Flores LLP
5 STREET: 4370 La Jolla Village Drive, Suite 700
6 CITY: San Diego
7 STATE: California
8 COUNTRY: USA
9 ZIP: 92122
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Floppy disk
12 COMPUTER: IBM PC compatible
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14 SOFTWARE: PatentIn Release #1.0, Version #1.25
15 CURRENT APPLICATION DATA: /na/na41.raa
16 APPLICATION NUMBER: us/na/na41.raa
17 FILING DATE:
18 CLASSIFICATION:
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: US 08/837,058
21 FILING DATE: 11-APR-1997
22 ATTORNEY/AGENT INFORMATION:
23 NAME: Campbell, Cathryn A.
24 REGISTRATION NUMBER: 31,815
25 REFERENCE/POCKET NUMBER: P-PM 3006
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: (619) 535-9001
28 TELEFAX: (619) 535-8949
29 INFORMATION FOR SEQ ID NO: 4:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 218 amino acids
32 TYPE: amino acid
33 TOPOLOGY: linear
34 FEATURE:
35 NAME/KEY: Peptide
36 LOCATION: 1..218
37 OTHER INFORMATION: /note="product = Human Histone
38 OTHER INFORMATION: H1-S-4"
39 US-09-041-889-4

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Query Match 54.9%; Score 45; DB 3; Length 218;

Best Local Similarity 57.1%; Pred. No. 13;

Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 PPKKKKSPKSK 16

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DB 146 PPKSAKTPPKAKK 159

Search completed: March 3, 2003, 06:15:50

Job time: 10.1463 secs

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DR EMBL; X85754; CAA59755.1; --
DR HSSP; P01112; IPLL.
DR InterPro; IPR001377; GTPase pas.
DR InterPro; IPR001230; Prenyl site.
DR InterPro; IPR001806; Ras trnsfrmg.
DR InterPro; IPR005225; Small GTP.
DR Pfam; PF00071; ras; 1.
DR PRINTS; PR00449; RASTNSFRMNG.
DR SMART; SM00173; RAS; 1.
DR TIGRFAMs; TIGR00231; small GTP; 1.
ZW Pfam; Pfam00071; GTP-binding; Prenylation; Lipoprotein.
FT NP_BIND 10 17 GTP (BY SIMILARITY).
FT NP_BIND 57 61 GTP (BY SIMILARITY).
FT NP_BIND 116 119 GTP (BY SIMILARITY).
FT DOMAIN 32 40 EFFECTOR REGION (BY SIMILARITY).
FT LIPID 185 185 FARNESYL (BY SIMILARITY).
SQ SEQUENCE 188 AA; 21452 MW; AABSC198B259865 CR64;

Query Match 95.7% Score 67; DA 1; Length 188;
Best local similarity 92.1%; Freq. NO. 0.0044;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEDSXXXXXXXXXX 14
DB 171 SEDSXXXXXXXXXX 184

RESULT 4
PASK_CYPCA STANDARD; PRT; 188 AA.
AC Q9YH38; 2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transforming protein p21 (K-Ras) (K1-Pas).
GN KRAS.
OS Cyprinus carpio (Common carp). Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Chang M.S., Chang Y., Chang G.D., Huang F.H., Huang M.J.,
PT "Molecular cloning and sequencing of two carp cDNAs encoding ras
PT related proteins."
RE submitted (APPENDED) to the EMBL/GenBank/DBP databases.
TI FUNCTION: RAS (RAS) IS A GTP-BINDING PROTEIN THAT IS INVOLVED IN
CC ACTIVITY.
CC -- PRTY: REGULATION: ALTERNATE BETWEEN AN INACTIVE FORM BOUND TO GDP
CC AND AN ACTIVE FORM BOUND TO GTP. ACTIVATED BY A GUANINE
CC NUCLEOTIDE-EXCHANGE FACTOR (GEF) AND INACTIVATED BY A PHASE
CC ACTIVATING PROTEIN (GAP).
CC -- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RAS FAMILY.
CC
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CC or send an email to license@sib-sib.ch).

DR EMBL; U53782; AAC05839.1; --
DR HSSP; P01112; IPLL.

CC use pas.
CC Prenyl site.
CC trnsfrmg.
CC Small GTP.
CC RAS.
CC all GTP; 1.
CC Prenylation; GTP binding;
CC GTPase activation
CC GTP.
CC GTP.
CC EFFECTOR REGION.
CC HYPERVARIABLE REGION.
CC FARNESYL.
CC G > C (IN LINE "PRTY").
CC /FTID=VAR 00044;
CC G > V (IN LINE "PRTY").
CC /FTID=VAR 00044;
CC C > H (IN LINE "AS IN MA PR310 AND
CC PANCEAS TM 4).
CC /FTID=VAR 00044;
CC P > A; LOSS OF GTP-BINDING ACTIVITY.
CC 14 WW; B1B6D189B83401 19047;

Query Match 95.7% Score 70; DA 1; Length 188;
Best local similarity 92.1%; Freq. NO. 0.0044;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEEDSXXXXXXXXXX 14
DB 171 SEDSXXXXXXXXXX 184

RESULT 4
PASK_CYPCA STANDARD; PRT; 188 AA.
AC Q9YH38; 2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transforming protein p21 (K-Ras) (K1-Pas).
GN KRAS.
OS Cyprinus carpio (Common carp). Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Chang M.S., Chang Y., Chang G.D., Huang F.H., Huang M.J.,
PT "Molecular cloning and sequencing of two carp cDNAs encoding ras
PT related proteins."
RE submitted (APPENDED) to the EMBL/GenBank/DBP databases.
TI FUNCTION: RAS (RAS) IS A GTP-BINDING PROTEIN THAT IS INVOLVED IN
CC ACTIVITY.
CC -- PRTY: REGULATION: ALTERNATE BETWEEN AN INACTIVE FORM BOUND TO GDP
CC AND AN ACTIVE FORM BOUND TO GTP. ACTIVATED BY A GUANINE
CC NUCLEOTIDE-EXCHANGE FACTOR (GEF) AND INACTIVATED BY A PHASE
CC ACTIVATING PROTEIN (GAP).
CC -- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RAS FAMILY.
CC
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DR EMBL; U53782; AAC05839.1; --
DR HSSP; P01112; IPLL.

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DR InterPro, IPR001077, GTPase Ras.
DR InterPro, IPR001210, Prenyl site.
DR InterPro, IPR001806, Ras transfmng.
DR InterPro, IPR001845, Small_GTP.
DR Pfam, PF00071, Ras_1.
DR PRINTS, PR00449, RASTRANSFMNG.
DR SMART, SM00173, RAS, 1.
DR TIGRFAMs, TIGR00231, small_GTP, 1.
KW PDEB-Substrate, GTP-binding, Prenylation, Hsp-protein
FT NP_BIND 16 17 GTP (BY SIMILARITY).
FT NP_BIND 57 61 GTP (BY SIMILARITY).
FT NP_BIND 116 119 GTP (BY SIMILARITY).
FT DOMAIN 32 40 EFFECTOR REGION (BY SIMILARITY).
FT LIPID 185 185 FARNESYL (BY SIMILARITY).
FT SEQUENCE 188 AA, 21454 MW, 255218DAF359659 CRC64.

Query Match 94.3%; Score 66; DB 1; Length 188;
Best Local Similarity 92.9%; Pred No. 0.0661;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEDGKFKFKFKSKTK 14
   |||:|||||
DB 171 SPGKFKFKFKSKTK 194

RESULT 5
RASK ORYLA
IF RASK ORYLA STANDARD, FFT, 199 AA
AC C42267,
DT 30 MAY-2000 (Rel. 39, Created)
DT 30 MAY-2000 (Rel. 39, Last sequence update)
DT 30 MAY-2000 (Rel. 39, Last sequence update)
CE Transformed Protein, P0/P-Ras-1 (P-Ras)
GN KRAS1.
OS Crystallin (Mollusca fish) (Japanese ricefish)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Cyprinodontiformes; Teleostei; Euteleostei;
OC Acanthopterygii; Atherinomorpha; Atherinomorpha; Atherinomorpha;
OC Belontiiformes; Atherinomorpha; Atherinomorpha; Atherinomorpha;
OC Rask_1 (taxid:8695);
CX 1
(1)
SEQUENCE FROM N.A.
KE TISSUE=Liver;
SA Clepper, G.L., Van Beneden, S.J.,
BT Volting of Ras-1 Ki-Ras GTPase sequences and a putative Ras-1 gene
RL Submitted (Oct 1997) to the EMBL/GenBank/DDBJ databases
CC 1. FUNCTION: RAS PROTEIN BINDS GTP AND EXCHANGES INTRINSIC GTPASE
CC ACTIVITY.
CC 2. ENZYME REGULATION: ALTERNATE BETWEEN AN INACTIVE FORM BINDING TO GTP
CC AND AN ACTIVE FORM BINDING TO GDP. ACTIVATED BY A GUANINE
CC NUCLEOTIDE EXCHANGE FACTOR (GEF) AND INACTIVATED BY A GTPASE-
CC ACTIVATING PROTEIN (GAP).
CC 3. SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY RAS FAMILY.
CC
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CC
DR EMBL: AF030545; AAB86487.1; -.
DR HSRP; P01177; fcll.
DR InterPro, IPR001077, GTPase Ras.
DR InterPro, IPR001210, Prenyl site.
DR InterPro, IPR001806, Ras transfmng.
DR InterPro, IPR001845, Small_GTP.
DR Pfam, PF00071, Ras_1.
DR PRINTS, PR00449, RASTRANSFMNG.
DR SMART, SM00173, RAS, 1.
DR TIGRFAMs, TIGR00231, small_GTP, 1.

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KW PDEB-Substrate, GTP-binding, Prenylation, Hsp-protein.
FT NP_BIND 16 17 GTP (BY SIMILARITY).
FT NP_BIND 57 61 GTP (BY SIMILARITY).
FT NP_BIND 116 119 GTP (BY SIMILARITY).
FT DOMAIN 32 40 EFFECTOR REGION (BY SIMILARITY).
FT LIPID 185 185 FARNESYL (BY SIMILARITY).
FT SEQUENCE 188 AA, 21450 MW, 2421871AA4722AA CRC64.

Query Match 94.3%; Score 66; DB 1; Length 188;
Best Local Similarity 92.9%; Pred No. 0.0661;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEDGKFKFKFKSKTK 14
   |||:|||||
DB 171 SPGKFKFKFKSKTK 184

RESULT 6
RASK MOUSE
IF RASK MOUSE STANDARD, PRT, 188 AA.
AC P08643; P04200;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transforming protein p21b (K-Ras 2b) (K-Ras) (c-K-ras).
GN KRAS2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
(1)
SEQUENCE FROM N.A.
KE TISSUE=Liver;
SA George, D.L., Scott, A.F., Trusko, S.J., Glick, B., Ford, E., Doherty, D.C.;
BT "Structure and expression of amplified c-Ki-ras gene sequences in Y1
RT mouse adrenal tumor cells."
RT Science 225:1159-1162(1984).
RN 1[1]
(2)
SEQUENCE OF 1-37 FROM N.A.
EX MEDLINE=8306333; PubMed=17474163;
RA Guerrero, I., Villasante, A., Corcos, V., Pellicer, A.;
RT "Activation of a c-Ki-ras oncogene by somatic mutation in mouse
RT lymphomas induced by gamma radiation."
RT Science 225:1159-1162(1984).
RN 1[3]
SEQUENCE OF 1-103 FROM N.A.
EX MEDLINE=8306333; PubMed=17474163;
RA Guerrero, I., Villasante, A.F., de Melville, B., Francke, U.;
RT "Amplified DNA in Y1 mouse adrenal tumor cells: isolation of c-Ki-ras
RT complementary DNA and activation of c-Ki-ras gene and localization of
RT coding of c-Ki-ras gene to mouse chromosome 6."
RN 1[4]
REVIEW.
RP MEDLINE=87297453; PubMed=3304147;
RX Barltis, W.
RT "Ras genes."
PL Annu. Rev. Biochem. 56:779-827(1987).
CC 1. FUNCTION: RAS PROTEIN BINDS GTP AND EXCHANGES INTRINSIC GTPASE
CC ACTIVITY.
CC 2. ENZYME REGULATION: ALTERNATE BETWEEN AN INACTIVE FORM BINDING TO GTP
CC AND AN ACTIVE FORM BINDING TO GDP. ACTIVATED BY A GUANINE
CC NUCLEOTIDE EXCHANGE FACTOR (GEF) AND INACTIVATED BY A GTPASE-
CC ACTIVATING PROTEIN (GAP).
CC 3. SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY RAS FAMILY.
CC
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CC
DR EMBL: AF030545; AAB86487.1; -.
DR HSRP; P01177; fcll.
DR InterPro, IPR001077, GTPase Ras.
DR InterPro, IPR001210, Prenyl site.
DR InterPro, IPR001806, Ras transfmng.
DR InterPro, IPR001845, Small_GTP.
DR Pfam, PF00071, Ras_1.
DR PRINTS, PR00449, RASTRANSFMNG.
DR SMART, SM00173, RAS, 1.
DR TIGRFAMs, TIGR00231, small_GTP, 1.

```


10 new genes KIAA1121-KIAA1129 deduced by
from human cell line K562;

11 N.A.

12 9492293;

13 "after L., N. and A.L. Williams F.

14 lies within 20 kb upstream of UBE1 in

15 "X inactivation center".

16 BELONGS TO RNA HCM BINDING, WITH A PREFERENCE
17 FOR AND LITTLE FOR POLY(A) BY SIMILARITY.

18 "Nuclear (by similarity)

19 1 PATCH DOMAIN

20 1 PAREP-TYPE ZINC FINGER

21 2 RNA RECOGNITION MOTIF (RPM)

22 ONE DIFFERS FROM THAT SHOWN HERE TO A

23 "N 493.

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29 entities requires a license agreement (see <http://www.ebi.ac.uk/submit/>
30 or send an email to license@ebi.ac.uk).

31 EMBL; U31351; AAB97618.1; .

32 FLYBASE; FBgn001087; g.

33 InterPro; IPR002553; Adaptin_N.

34 Pfam; PF01602; Adaptin_N_1.

35 SQ SEQUENCE 810 AA; 90159 MW; 019410R/DIEA-62 CRG64;

Query Match 71.4%; Score 50; DB 1; Length 410;
Best Local Similarity 81.3%; Pred. No. 4.2;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SKDCKKKKKKK 12

DB 722 SPDGKPKPKPK 733

RESULT 12

YD33 YEAST

ID YD33 YEAST

AC Q12117;

DT 30-MAY-2000 (Rel. 39, Created)

DI 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical 36.2 kDa protein in RAD28 LVS14 intergenic region.

CN YDR033W OR YD9673.03.

OS Saccharomyces cerevisiae (Baker's yeast).

CC Eukaryota, Fungi, Ascomycota, Basidiomycota, Basidiomycota, Ascomycota

CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RA Arnold W., Becker A., Jaeger W., Kuester H., Nussbaum P.

RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

EC STRAIN=S288C / AB072;

RA Connor P., Church G.M., Barrell B.G., Barandrea M.A., Walsh S.V.

PL Submitted (DEC 1996) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).

CC -1- SIMILARITY: BELONGS TO THE ARCHAEAL OPSIN FAMILY. Belongs

CC SUBFAMILY.

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DR InterPro: IPR000504; RNA_rec_mot.
DR InterPro: IPR000923; Znf_C2H2.
DR InterPro: IPR001876; Znf_FanGDP.
DR Pfam: PF00076; rrm; 2.
DR Pfam: PF00094; zf_C2H2; 1.
DR Pfam: PF00641; zf-RanBP; 1.
DR Pfam: PF01585; G_patch; 1.
DR SMART: SM00443; G_patch; 1.
DR SMART: SM00360; RRM; 2.
DR SMART: SM00355; Znf_C2H2; 1.
DR SMART: SM00547; Znf_PRR; 1.
DR PROSITE: PS00174; G_PATCH; 1.
DR PROSITE: PS00102; RRM; 2.
DR PROSITE: PS00030; RRM_RNP; 2.
DR PROSITE: PS01358; ZF_RANBP2; 1.
DR PROSITE: PS01199; ZF_RANBP2; 1.
EF FINGER, F55157, ZINC_FINGER_C2H2; 1.
KW Anti-oncogene; RNA-binding; Nucleic acid binding; Zinc finger; Repeat.
FT DOMAIN 98 178 RNA BINDING (PPM) 1.
FT ZN_FING 181 210 RANBP2 TYPE.
FT DOMAIN 231 315 RNA-BINDING (PPM) 2.
FT ZN_FING 647 677 C2H2-TYPE (ATYPICAL).
FT DOMAIN 743 789 G-PATCH.
FT CONFLICT 53 54 DY -> GS (IN REF. 1).
FT CONFLICT 354 354 G -> V (IN REF. 1).
FT CONFLICT 455 455 MISSING (IN REF. 6).
FT CONFLICT 788 788 G -> A (IN REF. 6).
FT CONFLICT 812 812 T -> I (IN REF. 1).
SQ SEQUENCE 815 AA, 92153 MW, AA799CD13405479 QRCQ64;

Query Match 65.78; Score 46; DB 1; Length 815;
Best Local Similarity 57.18; Pred No 15;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 SZDGKYYKYYKYYK 14
: : : : : : : : : :
DB 522 AVEGKREKREKPK 535

Search completed: March 3, 2003, 06:46:23
Job time : 5.95122 secs

DR EMBL; BC024153; AAH24153.1; -
 DR InterPro; IPR000457; G_patch.
 DR InterPro; IPR000504; RNA rec mot.
 L-106111; IPR000822; ZnF_RHG.
 DR InterPro; IPR001876; ZnF_RanGDP.
 DR Pfam; PF00076; rim_2.
 L1 Pfam; PF00047; Znf_RHG2.
 L2 Pfam; PF00641; Zf_RanBP.
 DR SMART; SM00443; G_patch.
 DR SMART; SM00160; RRM_2.
 DR SMART; SM03355; Znf_RHG2.
 DR SMART; SM00547; Znf_RHG2.
 DR PROSITE; PS0102; RRM_2.
 DR PROSITE; PS00649; RRM_RNP_1; TRNPNW.
 DR PROSITE; PS0199; Zf_RanBP.
 DR PROSITE; PS0197; ZINC_FINGER_CSD2_1.
 DR DNA-binding; ZINC_FINGER.
 KW SEQUENCE 330 AA; 10304 MW; 470F8F8F8F7A5734 CFC64.

Query Match: 75.7%; Score 53; DP 4; Length 930;
 Best Local Similarity: 71.4%; Pred. No. 5.5;
 Matches: 10; Conservative: 3; Mismatches: 1; Indels: 0; Gaps: 0;

Q7 1 SPGCKKKKKKKKKKK 14
 |||:|||||
 Db 633 SPGCKKKKKKKKKKK 646

RESULT 9
 Q9KX3 PRELIMINARY; PPT: 930 AA.
 ID Q9KX3;
 AC Q9KX3;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Similar to RNA binding motif protein 10.
 OS Mus musculus (Mouse)
 CC Eukaryota; Metazoa; Chordata; Cladibia; Vertebrata; Euteleostomi.
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strauberg R.
 RL Submitted (MAR 2001) to the EMBL/GenBank/DBP databases
 DR EMBL; BC004674; AA004674.1; -
 DR InterPro; IPR000467; G_patch.
 DR InterPro; IPR000504; RNA rec mot.
 DR InterPro; IPR000822; ZnF_CHE.
 DR InterPro; IPR001876; ZnF_RanGDP.
 DR Pfam; PF01585; G_patch; 1.
 DR Pfam; PF00076; rim_2.
 DR Pfam; PF00047; Znf_RHG2.
 DR Pfam; PF00641; Zf_RanBP.
 DR SMART; SM00443; G_patch; 1.
 DR SMART; SM00360; RRM_2.
 DR SMART; SM03355; Znf_RHG2.
 DR SMART; SM00547; Znf_RHG2.
 DR PROSITE; PS0102; RRM_2.
 DR PROSITE; PS00649; RRM_RNP_1; TRNPNW.
 DR PROSITE; PS0199; Zf_RanBP.
 DR PROSITE; PS0197; ZINC_FINGER_CSD2_1.
 DR DNA-binding; Zinc finger.
 KW SEQUENCE 330 AA; 10304 MW; 5FACAC7C6AF10A7 CFC64.

Query Match: 75.7%; Score 53; DP 11; Length 930;
 Best Local Similarity: 71.4%; Pred. No. 5.5;
 Matches: 10; Conservative: 3; Mismatches: 1; Indels: 0; Gaps: 0;

Q7 1 SPGCKKKKKKKKKKK 14
 |||:|||||
 Db 633 SPGCKKKKKKKKKKK 646

RESULT 10
 Q9FXB5 PRELIMINARY; PPT: 522 AA.
 ID Q9FXB5;
 AC Q9FXB5;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 21, Last annotation update)
 DE P25P12.91 protein.
 GN P25P12.91.
 OS Arabidopsis thaliana (Mouse-ear cress).
 CC Eukaryota; Viridiplantae; Streptophyta; Etrichordata; Tracheophyta;
 CC Spermatophyta; Magnoliopsida; Euphyllophytes; Core eudicots; Rosidae;
 CC Ericaceae; Primulales; Ericaceae; Arabidopsi.
 CX NCBI_TaxID=10709;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pedersen N.A., Palm C.J., Conway A.R., Conn L., Hanson N.F.,
 RA Altschul H., Nguyen M., Lam R., Southwick A., Bell, Ruchler E., Chin C.,
 RA Chiu J., Choi E., Papp P., Gonzalez A., Hwang B., Kim C., Koo T.,
 RA Lee J., Lee J., Lee J., Lee J., Lee J., Lee J., Lee J., Lee J.,
 RA Pham P., Sakano H., Schwartz J., Chinn P., Thayer A., Toriumi M.,
 RA Vayabeta M., Walker M., Yi G., Foker J., Theologis A., Davis R.W.
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBP databases.
 DR EMBL; AC000343; AAC000000.1; -
 DR PRINTS; PP01574; TURRYPROTEIN.
 DR SEQUENCE 522 AA; 60740 MW; 60AF1553761071PS CFC64;

Query Match: 74.3%; Score 50; DP 10; Length 522;
 Best Local Similarity: 71.4%; Pred. No. 4.7;
 Matches: 10; Conservative: 2; Mismatches: 2; Indels: 0; Gaps: 0;

Q7 1 SPGCKKKKKKKKKKK 14
 |||:|||||
 Db 424 SPGCKKKKKKKKKKK 437

RESULT 11
 O61747 PRELIMINARY; PPT: 455 AA.
 ID O61747;
 AC O61747;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Putative 45.9 kDa protein.
 GN B2205.10.
 OS Caenorhabditis elegans.
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 CC Phasmodia; Phasmodia; Caenorhabditis.
 CX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strauberg R.
 RL Submitted (MAY 1998) to the EMBL/GenBank/DBP databases.
 DR EMBL; AF067211; AAC16986.1; -
 DR Hypothetical protein
 KW SEQUENCE 455 AA; 46850 MW; 5FA5C18A322A4C24 CFC64;

Query Match: 75.7%; Score 53; DP 11; Length 930;
 Best Local Similarity: 71.4%; Pred. No. 5.5;
 Matches: 10; Conservative: 3; Mismatches: 1; Indels: 0; Gaps: 0;

Q7 1 SPGCKKKKKKKKKKK 14
 |||:|||||
 Db 633 SPGCKKKKKKKKKKK 646

5: Score 51; DB 5; Length 455;
 6: Pred. No. 5.8;
 7: Mismatches 0; Indels 0; Gaps 0;
 8: (Created)
 9: Last sequence update
 10: Last annotation update
 11: (Created)
 12: Last sequence update
 13: Last annotation update
 14: (Created)
 15: Last sequence update
 16: Last annotation update
 17: (Created)
 18: Last sequence update
 19: Last annotation update
 20: (Created)
 21: Last sequence update
 22: Last annotation update
 23: (Created)
 24: Last sequence update
 25: Last annotation update
 26: (Created)
 27: Last sequence update
 28: Last annotation update
 29: (Created)
 30: Last sequence update
 31: Last annotation update
 32: (Created)
 33: Last sequence update
 34: Last annotation update
 35: (Created)
 36: Last sequence update
 37: Last annotation update
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 90: Last sequence update
 91: Last annotation update
 92: (Created)
 93: Last sequence update
 94: Last annotation update
 95: (Created)
 96: Last sequence update
 97: Last annotation update
 98: (Created)
 99: Last sequence update
 100: Last annotation update

PP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 PA Wilken P., Ainsworth P., Anderson P., Payson C., Boileau M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper D., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin P., Favello A., Fothergill J.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Hirst M., Johnson L.,
 RA Jones M., Kershaw J., Kirsten J., Laister M., Latreille J.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shawcross P.,
 RA Smalton N., Smith A., Schnhammer E., Staden R., Sulston R.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Whitworth P.,
 RA Watson A., Weinstock L., Wilkinson-Spratt J., Weidman P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans."
 RL Nature 368:32-38(1994).
 RN (2).
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Wilcox L.;
 RT "The sequence of C. elegans cosmid C10B12."
 PL Submitted (JAN-1997) to the EMBL/GenBank/DBPJ databases.
 RN (3).
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBPJ databases.
 DR EMBL; U00032; AAB53978.1; .;
 SQ SEQUENCE 552 AA; 62427 MW; 2530775E3D7ED394 CPO44;
 Query Match 71.4%; Score 50; DB 5; Length 452;
 Best Local Similarity 78.6%; Pred. No. 9.7;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 SKGGKYYKYYKTK 14
 DB 115 SYDEKYYKYYKTK 138
 RESULT 14
 Q9VY96
 ID Q9VY96 PRELIMINARY; PRT; 568 AA.
 AC Q9VY96;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE CG1197 protein.
 GN G of CG10896 OP CG1197.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 CX NCBI_TaxID=7227;
 RN (1).
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M. D., Ceiniker S. E., Holt R. A., Evans C. A., Gocayne J. D.,
 RA Amanatides P. G., Scherer S. E., Li P. W., Hoskins R. A., Valle R. E.,
 RA George R. A., Lewis S. E., Richards S., Ashburner M., Hunkeler S. N.,
 RA Sutton G. G., Wortman J. P., Vandell M. D., Zhang C., Chen L. X.,
 RA Brandon R. C., Rogers Y.-H. C., Blazer V. S., Chapple M., Pfeiffer H. D.,
 RA Wan K. H., Doyle C., Baxter E. G., Holt R. A., Nelson C. P., McKler G. L. G.,
 RA Abril J. F., Aghayani A., An H.-J., Andrews-Blankenship R., Baldwin D.,
 RA Baller R. M., Basu A., Ravendale J., Bayraktaroglu L., Beasley E. M.,
 RA Benson K. Y., Bencos P. Y., Bertram E. F., Bhandari D., Bolshakov S.,
 RA Borokova N., Borchen M. P., Bouck J., Buckstein P., Brooker P.,
 RA Burtis K. C., Busam D. A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J. M., Cawley S., Dahlve C., Pavement L. B., Davies P.,
 RA de Fabes P., Selver A., Dadd C., Mays A., Dadd C., Mays A., Dadd C.,
 RA Dadd C., Mays A., Dadd C., Mays A., Dadd C., Mays A., Dadd C.,
 RA Durbin K. J., Evangelista C. C., Ferraz C., Ferreira S., Feisemann W.,
 RA Foster C., Gabriellian A. E., Garg N. S., Gelbart W. M., Glauser F.,

Job time : 33.3932 secs

EA Glick A., Eick P., Gerschlager H., Gu Z., Guo F., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.P., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kearnson A., Korchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 EA Nelson C.S., Nelson K.A., Nixon K., Nusskern D.P., Pacleb J.M.,
 RA Palacelis M., Pittman G.S., Pan S., Peillard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun F.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.F., Zaveri J.S., Zhang X., Zhang G., Zhao C., Zheng L.,
 RA Zhang X.H., Zhang F.H., Zhang W., Zhang X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 E1 C01828 287 2185 C195 (2000).
 DP EMBL: AE003493; AAF48107 1;
 DR FlyBase: FBgn001087; g.
 DR InterPro: IPR002553; Adaptin_N.
 DR Pfam: PF01602; Adaptin_N; 1.
 SQ SEQUENCE 568 AA; 63011 MW; C4F1507AAARH07AA CRC64;

Query Match 71.4%; Score 50; DB 5; Length 568;
 Best Local Similarity 83.3%; Pred No. 9 9;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SKDCKKPKKPK 12
 |||||
 DE 493 SKDCKKPKKPK 504

RESULT 15
 O45031
 ID O45031 PRELIMINARY; PRT: 810 AA.
 AC O45031;
 DT 01-JUN-1998 (TrEMBLrel 06, Created)
 DI 01-JUN-1998 (TrEMBLrel 06, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel 17, Last annotation update)
 DE Delta adaptin subunit of AP-3.
 OS G OR GARNER OR CGL096 OE CGL1197.
 OS Drosophila melanogaster (fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Insecta; Hexapoda; Insecta;
 CC Euryptera; Neptera; Euryptera; Euryptera; Euryptera;
 CC Euryptera; Neptera; Euryptera; Euryptera; Euryptera;
 CC Euryptera; Neptera; Euryptera; Euryptera; Euryptera;
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N A
 RC STRAIN=OREGON;
 RA Lloyd V.K., Sinclair D.A., Wennberg P., Warner T.S., Honda R.M.,
 RA Grigliatti T.A.; (1994) to the EMBL/GenBank/DBP1 databases
 RL Submitted (JAN 1994) to the EMBL/GenBank/DBP1 databases
 DE EMBL: AF044287; AAC01743.1;
 DE FlyBase: FBgn001087; g.
 DE InterPro: IPR002553; Adaptin_N
 DE Pfam: PF01602; Adaptin_N; 1;
 SQ SEQUENCE 410 AA; 40066 MW; E3010657R88R8P54R CRC64;

Query Match 71.4%; Score 50; DB 5; Length 810;
 Best Local Similarity 83.3%; Pred No. 14;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SKDCKKPKKPK 12
 |||||
 DE 722 SKDCKKPKKPK 733

XX PS Claim 11; Page 70; 75pp; English.

XX CC The present peptide sequence represents a specifically claimed membrane

XX CC binding element. The invention relates to a soluble derivative (A) of a

XX CC soluble polypeptide (I), which comprises at least 2 heterologous

XX CC membrane-binding elements (MKE) of low membrane affinity covalently

XX CC associated with (i) MRE interact, independently and with thermodynamic

XX CC affinity, with components of cellular or artificial membranes exposed

XX CC to extracellular fluids (A) are used to treat disorders treatable with

XX CC (i) itself, specifically inflammation or any other complement related

XX CC disorder (e.g. connective tissue disease, graft rejection, myocardial

XX CC infarction, sepsis, thrombotic arthritis and many others, including

XX CC application to immobilizing devices and therapy in disease, but also,

XX CC treatment, induce weight loss, to treat ischemia or asthma and as

XX CC immunomodulators for treating multiple sclerosis (A) are administered

XX CC orally, topically, by injection or inhalation at 0.1 to preferably

XX CC 0.1-10) mg/kg/day.

XX CC

XX CC Sequence 14 AA,

XX CC

Query Match 100.0%; Score 70; DP 19; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00042;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFFGKFFKFFKFFKFF 14

DB 1 CFFGKFFKFFKFFKFF 14

RESULT 2

ABB91241

ID ABB91241 standard; peptide; 14 AA.

XX AC ABB91241;

XX DT 20 AUG 2002 (first entry)

XX DE Antibacterial membrane binding peptide SEQ ID NO 9

XX KW Antibacterial, glycopeptide, peptide reagents associated with

XX KW bacterial infection; vancomycin; peptidoglycan biosynthesis inhibition;

XX KW antibiotic.

XX OS Synthetic.

XX PS WO200236612 A1.

XX PD 10 MAY 2002.

XX PF 02 NOV 2001; 2001WO560467

XX PR 03 NOV 2000; 2000RP 0006024.

XX PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX PA (ADPR-) ADPRUTECH LTD.

XX PI Coufal X3, Bailey CE,

XX DP WPI; 2002 471499/50.

XX PT Antibacterial compound, useful for the treatment of a bacterial

XX PT infection by administration of negative bacteria, variants 9

XX PT conjugate of glycopeptide and peptide membrane associating element

XX PS Claim 7; Page 57; 64pp; English.

XX CC The present invention describes an antibacterial compound (I), comprising

XX CC a conjugate of glycopeptide and peptide membrane associating element

XX CC (I) comprises the formula V, X, Y, Z, where V is a glycopeptide moiety that

XX CC inhibits peptidoglycan biosynthesis in bacteria, X is a binding group,

XX CC W is a peptide membrane associating element, and Y is a membrane

XX CC insertive element. Also described is (i) a method of treating or preventing

XX CC a bacterial infection, comprising the administration of (I) and (ii) use

XX CC of (i) in the manufacture of a medicament for the treatment or prevention

XX CC of a bacterial infection. (ii) are used in the manufacture of a medicament

XX CC for the treatment or prophylaxis of a bacterial infection in a human or

XX CC animal body, including both the upper digestive and gram negative bacteria

XX CC including *Mycobacterium* sp., *Enterococcus* sp., *Escherichia* sp.,

XX CC *Staphylococcus* sp., *Vibrio* sp., *Helicobacter* sp., *Portella* sp., *Klebsiella*

XX CC sp., *Hemophilus* sp., *Clostridium* sp., *Pseudomonas* sp., *Aspergillus* sp.,

XX CC *Phanerochaete* sp., *Saccharomyces* sp., particularly antifungal resistant

XX CC bacterial strains. (iii) are also useful in wound treatment agents to

XX CC prevent bleeding of bacteria in medical devices, especially for treating

XX CC exposed in wound tissues, and for prophylactic use in dental treatment as

XX CC an alternative to, or in combination with, antibiotic prophylaxis. (iv)

XX CC has stronger binding to bacterial membrane which have a higher

XX CC content of acidic phospholipids than the ordinary membrane, also

XX CC having a higher proportion of membrane associated fluorescent proteins.

XX CC Various other advantages and industrial activity upon derivation

XX CC with (i) and is effective to treat the antibiotic resistant bacterial

XX CC strains. ABB91234 to ABB91292 represent peptides given in the

XX CC exemplification of the present invention.

XX CC

XX CC Sequence 14 AA,

XX CC

Query Match 100.0%; Score 60; DP 23; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00042;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CFFGKFFKFFKFFKFF 14

DB 1 CFFGKFFKFFKFFKFF 14

RESULT 3

AAW45893

ID AAW45893 standard; peptide; 15 AA.

XX AC AAW45893;

XX DT 30 JUN 1998 (first entry)

XX DE Peptide membrane binding element.

XX KW Membrane binding element, thrombin disease, soluble protein;

XX KW complement-related disease; integral membrane protein; inflammation.

XX OS Synthetic.

XX PS WO9802454-A2.

XX PD 22 JAN 1998.

XX PF 08 JUL 1997; 97WO-EP03715.

XX PP 15 JUL 1996; 96GR-0014871.

XX PA (ADPR-) ADPRUTECH PLC.

XX PI Coufal X3, Wenzel-Werk DEI, Smith RAG;

XX DP WPI; 1998 110524/10.

XX PT Derivatives of soluble poly-peptide(s) bonded to low affinity

XX PT membrane binding group, useful for treating complement related and

XX PT thrombin diseases, providing improved localization at cellular

XX PT membranes

XX PS Claim 21; Page 71; 75pp; English.

XX CC The present peptide sequence represents a specifically claimed membrane

XX CC binding element. The invention relates to a soluble derivative (A) of a

XX CC soluble polypeptide (I), which comprises at least 2 heterologous

XX CC membrane-binding elements (MKE) of low membrane affinity covalently

XX CC associated with (i) MRE interact, independently and with thermodynamic

XX CC affinity, with components of cellular or artificial membranes exposed

XX CC to extracellular fluids (A) are used to treat disorders treatable with

XX CC (i) itself, specifically inflammation or any other complement related

XX CC disorder (e.g. connective tissue disease, graft rejection, myocardial

XX CC infarction, sepsis, thrombotic arthritis and many others, including

XX CC application to immobilizing devices and therapy in disease, but also,

XX CC treatment, induce weight loss, to treat ischemia or asthma and as

XX CC immunomodulators for treating multiple sclerosis (A) are administered

XX CC orally, topically, by injection or inhalation at 0.1 to preferably

XX CC 0.1-10) mg/kg/day.

AAW58548
ID AAW58548 standard; peptide; 18 AA.
AC
XX
AC AAW58548;
XX
XX
DT 03-SEP-1998 (first entry)
DE K-Pas4B farnesylation signal peptide
XX
XX
DE H-Ras; cell compartment localisation domain, plasma membrane, farnesylation; palmitoylation; myristoylation; signal; drug screening; protein recruitment system, protein-protein interaction.
XX
XX
OS Homo sapiens.
XX
PN US5776683-A.
XX
PD 07-JUL-1998.
XX
XX 19-JUL-1996; 94US-0683877.
XX
XX 19-JUL-1996; 94US-0683877.
XX
XX (BAYU) BAYLOR COLLEGE MEDICINE.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Aronheim A, Elledge SJ, Karin M,
XX
XX P1
XX
XX WPI; 1998-198022/34.
XX
XX
PT Identifying protein-protein binding using protein recruitment system
PT - involving two fusion proteins, one containing effector and the
PT other membrane localisation domain, particularly for screening cDNA
PT expression libraries for potential therapeutic agents
XX
XX
PS Disclosure; Colomo A, 1999, English.
XX
XX A method has been developed for identifying protein-protein binding using
XX a protein recruitment system. The method comprises: (a) expressing in a
XX cell, a first nucleic acid (i) encoding a fusion protein (FP) comprising
XX an effector protein (EP), which is not a transcription factor, and a
XX target protein (TP), (b) expressing in the same cell a second nucleic
XX acid (ii) encoding a fusion protein (FP2) comprising a cell membrane
XX localisation domain (CMD) and a second protein (SP) and (c) detecting
XX activation of a reporter gene (RPG) by detecting a signal that
XX identifies binding between TP and SP. The present sequence represents a
XX cell compartment localisation domain useful in the invention. The method
XX is used to identify SP, e.g. from a cDNA expression library, and also for
XX screening compounds (potential therapeutic agents) that modulate the
XX protein-protein interaction. The method may also be used for analysing
XX interaction between 3 proteins, e.g. where one bridges the interaction
XX between the other two. Unlike the conventional 2 hybrid assay, this
XX method allows study of proteins with powerful transcriptional activity,
XX and it detects interaction in the cellular compartments (not just the
XX nucleus) where these occur naturally, e.g. after post-translational
XX modification. The inexpressible false positives encountered in the
XX 2-hybrid assay should not occur with the new system.
XX
SQ Sequence 18 AA;
Query Match 100.0%; Score 70; DB 21; Length 18;
Best Local Similarity 100.0%; Prev No 6 00058;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 SKDGRYKFFKFFKFFK 14
| | | | | | | | | |
DB 1 SKDGRYKFFKFFKFFK 14
RESULT 7
AAU99126
ID AAW99126 standard; Peptide; 20 AA.
XX

AAU99126;
24-SEP-2002 (first entry)
K-Pas membrane localisation signal.
K-Pas, membrane localisation signal; membrane molecule indicator;
membrane molecule.
Unidentified.
W0000244700 A2.
06-JUN-2002.
29-NOV-2001; 2001WO 0113952.
30 NOV 2000; 2000US 250679P.
18 DEC-2000; 2000US-256559P.
(HECA) NETHERLANDS CANCER INST.
Jalink K;
WPI; 2002 527337/56.
Membrane molecule indicator for determining a property of a membrane
molecule and identifying modulators of a property of a membrane
molecule, comprises a membrane molecule indicator domain, and donor and
acceptor fluorescent domains
Example 1; Page 49; 94pp; English.
This invention relates to a novel membrane molecule indicator comprising
a membrane molecule indicator domain, a donor fluorescent domain, and an
acceptor fluorescent domain, where fluorescence resonance energy
transfer (FRET) between the donor domain and the acceptor domain is
indicative of a property of membrane molecule. A cell comprising a
membrane molecule indicator is useful for determining a property of a
membrane molecule in a cell, by providing the cell and determining
FRET between the donor fluorescent domain and acceptor fluorescent
domain, where the cell expresses a known or candidate signaling
molecule such as a protein coupled receptor. A cell comprising the
membrane molecule indicator is also useful for identifying a compound,
preferably a receptor antagonist, antagonist of inverse agonist, that
modulates a property of a membrane molecule by administering the test
compound to the cell. If the cell exhibits a reduction in expression of the
test compound in the cell. A membrane indicator molecule is useful to
identify and determine the function of modulators of cellular signalling
pathways and has therapeutic, diagnostic and research applications. The
membrane indicator molecule and the above method are useful for
expressing cloning of new modulators that affect the abundance,
localisation, conformation or post-translational modification state of
the membrane molecule of interest, for determining the function of
various signalling molecules, such as single nucleotide polymorphisms, disease
associated mutations and engineered variations in receptors and
effectors), establishing dose-response curves of modulators of membrane
molecules and for detecting alterations in membrane molecules and
modulators that reflect disease state, which can be applied to the
development of diagnostic methods. The present sequence represents
an invention.
Sequence 20 AA;
Query Match 100.0%; Score 70; DB 21; Length 20;
Best Local Similarity 100.0%; Prev No 6 00058;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 SKDGRYKFFKFFKFFK 14
| | | | | | | | | |
DB 3 SKDGRYKFFKFFKFFK 16

Matches 14, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
 QY 1 SPDSPPPPPPPTTF 14
 II 4 SPDSPPPPPPPTTF 14
 DB 4 SPDSPPPPPPPTTF 14
 RESULT 10
 AAB67662
 ID AAB67662 standard; peptide; 21 AA.
 XX
 AC AAB67662;
 DT 11-JUN-2001 (first entry)
 DE K ras peptide which is a substrate for farnesyl transferase
 XX
 FW Farnesyl transferase, a carboxyl chroman, cellular proliferation, cancer,
 psoriasis, restenosis, tumor; Kaposi sarcoma, carcinoma; Wilms tumor,
 chondrosarcoma, chondrosarcoma, chondrosarcoma, chondrosarcoma, chondrosarcoma,
 melanoma, multiple myeloma, chronic lymphocytic leukemia, glioma,
 melanoma, granulocytic lymphoma, ras oncogene, K-ras.
 XX
 CC Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Modified-site 1 /note "biotinylated beta-alanine"
 FT Modified-site 2 /note "beta-alanine"
 FT Modified-site 3 /note "beta-alanine"
 FT Modified-site 3 /note "beta-alanine"
 XX WC200109124 A1.
 PN 08-FEB-2001.
 XX
 XX 28 JUN-2000, 2000WC-FEB0193.
 XX 30 JUN-2000, 2000WC-FEB0201.
 XX (AVET) AVENTIS PHARMA SA.
 XX Baudouin B, Jimonet P,
 XX WPI; 2001 24470/24.
 XX New 4 (imidazolylalkylamino) chroman-8 carboxamide derivatives, are
 PT farnesyl transferase inhibitors useful for treating hyperproliferative
 PT disorders, e.g. psoriasis, restenosis or especially cancer -
 XX
 XX Example 20A, Page 51, Table, French.
 XX
 CC The present sequence represents a peptide which is representative of
 CC K-ras, and which is acts as a substrate for farnesyl transferase. The
 CC enzyme transfers a farnesyl group to the cysteine residue of the present
 CC peptide in the presence of farnesyl pyrophosphate (FPP). The
 CC specification describes a farnesyl chroman-8 carboxamide which inhibit
 CC farnesyl transferase. The farnesyl transferase inhibitors are used for
 CC treating diseases associated with signal pathways involving farnesyl
 CC transferase and cellular proliferation, especially cancer. More
 CC generally, they are useful in the treatment of diseases involving
 CC malignant or benign cellular proliferation, including psoriasis,
 CC restenosis, solid tumors, Kaposi sarcoma, chondrosarcoma, chondrosarcoma,
 CC chondrosarcoma, neuroblastoma, Wilms tumor, Hodgkin's disease,
 CC melanoma, teratocarcinoma, glioma, multiple myeloma, chronic lymphocytic
 CC leukemia, chondrosarcoma, glioma, chondrosarcoma, chondrosarcoma,
 CC chondrosarcoma, chondrosarcoma, chondrosarcoma, chondrosarcoma, chondrosarcoma,
 CC melanoma, multiple myeloma, chronic lymphocytic leukemia, glioma,
 CC melanoma, granulocytic lymphoma, ras oncogene, K-ras.
 CC The inhibitors are especially useful for
 CC treating cancers expressing the activated ras oncogene.

Every March 100.0%; Score 70; US 22; Length 21;
 Best Local Similarity 100.0%; Pred No 0.00061;
 March 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SPDSPPPPPPPTTF 14
 II 4 SPDSPPPPPPPTTF 14
 DB 4 SPDSPPPPPPPTTF 17
 RESULT 11
 AAB67665
 ID AAB67665 standard; peptide; 21 AA.
 XX
 AC AAB67665;
 DT 11-JUN-2001 (first entry)
 DE F ras peptide which is a substrate for farnesyl transferase.
 XX
 FW Farnesyl transferase, a carboxyl chroman-8 carboxamide derivatives, are
 psoriasis, restenosis, tumor; Kaposi sarcoma, carcinoma; Wilms tumor,
 chondrosarcoma, chondrosarcoma, chondrosarcoma, chondrosarcoma, chondrosarcoma,
 melanoma, multiple myeloma, chronic lymphocytic leukemia, glioma,
 melanoma, granulocytic lymphoma, ras oncogene, K-ras.
 XX
 CC Synthetic
 XX
 PH Key Location/Qualifiers
 FT Modified-site 1 /note "biotinylated beta-alanine"
 FT Modified-site 2 /note "beta-alanine"
 FT Modified-site 3 /note "beta-alanine"
 FT Modified-site 3 /note "beta-alanine"
 XX WC200109125-A1.
 PN 08-FEB-2001.
 XX
 XX 28 JUN-2000, 2000WC-FEB0193.
 XX 30 JUN-2000, 2000WC-FEB0201.
 XX (AVET) AVENTIS PHARMA SA.
 XX Baudouin B, Jimonet P, Maigret S, Aillard B, Mailliet P, Laou A,
 XX Nemecek C,
 XX WPI; 2001 24470/24.
 XX New 4 (imidazolylalkylamino) chroman-8 carboxamide derivatives, are
 PT farnesyl transferase inhibitors useful for treating hyperproliferative
 PT disorders, e.g. psoriasis, restenosis or especially cancer -
 XX
 XX Disclosure; Page 1; 13pp; French
 XX
 CC The present sequence represents a peptide which is representative of
 CC K-ras, and which is acts as a substrate for farnesyl transferase. The
 CC enzyme transfers a farnesyl group to the cysteine residue of the present
 CC peptide in the presence of farnesyl pyrophosphate (FPP). The
 CC specification describes a farnesyl chroman-8 carboxamide which inhibit
 CC farnesyl transferase. The farnesyl transferase inhibitors are used for
 CC treating diseases associated with signal pathways involving farnesyl
 CC transferase and cellular proliferation, especially cancer. More
 CC generally, they are useful in the treatment of diseases involving
 CC malignant or benign cellular proliferation, including psoriasis,
 CC restenosis, solid tumors, Kaposi sarcoma, chondrosarcoma, chondrosarcoma,
 CC chondrosarcoma, neuroblastoma, Wilms tumor, Hodgkin's disease,
 CC melanoma, teratocarcinoma, glioma, multiple myeloma, chronic lymphocytic
 CC leukemia, chondrosarcoma, glioma, chondrosarcoma, chondrosarcoma,
 CC chondrosarcoma, chondrosarcoma, chondrosarcoma, chondrosarcoma, chondrosarcoma,
 CC melanoma, multiple myeloma, chronic lymphocytic leukemia, glioma,
 CC melanoma, granulocytic lymphoma, ras oncogene, K-ras.
 CC The inhibitors are especially useful for
 CC treating cancers expressing the activated ras oncogene.

DE Human colon cancer antigen protein SEQ ID NO 4146.
XX
XX Human colon cancer antigen; diagnosis; detection;
XX colorectal carcinoma; chromosome 12
OS
XX Homo sapiens.
XX
XX W520312290 A2.
XX
XX 05-APR-2001.
XX
XX 24 SEP 2000; 000000 W520524
XX
XX 23-SEP-1999; 000000 W52147
XX 03-NOV 1999; 9905-0163280.
XX (HWA) HUMAN GENOME SCI INC
XX
XX Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
XX WPI; 2001-235357/24.
XX N PDBE, AAH33013.
XX
XX The following are 300-4000 human colon cancer associated polypeptides,
XX useful for preventing, diagnosing and/or treating colorectal cancers -
XX
XX Claim 1; Page 6186; 9903pp, English.
XX
XX AAH33013. AAH33014 to AAH33016 represent human colon
XX cancer associated polypeptides (P) and proteins (P), where
XX the proteins are collectively known as colon cancer antigens. The colon
XX cancer antigens have cytostatic activity and can be used in gene
XX therapy and vaccine production. N and P may be used in the prevention,
XX diagnosis and treatment of diseases associated with inappropriate P
XX expression. For example, N and P may be used to treat diabetes
XX associated with increased expression by rectifying mutations of beta
XX in a patient's genome that affect the activity of P by expressing
XX inactive proteins or to supplement the patient's own production of P.
XX Alternatively, N may be used to reduce the colon cancer associated P
XX by inserting the nucleic acids into a host cell and culturing the cell
XX to express the protein. N and P can be used in the prevention, diagnosis
XX and treatment of colorectal carcinomas and cancers. AAH33014 to AAH33016
XX and AAH33018 represent sequences used in the exemplification of the
XX present invention.
XX N.B. Pages 666 to 682 and page 7053 of the sequence listing were
XX missing at time of publication, meaning no sequences are present for
XX SEQ ID NO:1027 to 1052, 9921 and 9922.
XX
XX Sequence 92 AA;

Query Match 100.0%, Score 35; DB 22; Length 92;
Best Local Similarity 100.0%; Prod No. 0.0024;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPGQYKYYKYYKYYK 14
D6 75 SPGQYKYYKYYKYYK 88

RESULT 15
AAW04473
ID AAW04473 standard; Protein; 188 AA.

XX
XX AAW04473;

XX
XX 05-AUG-1997 (first entry)

XX Human K-ras B protein isoform.

XX
XX Farnesyl transferase, inhibitor; cancer, tumor, neoplasia; farnesyl
XX ras protein; K-ras B; malignant; detection; identification.
XX
XX Homo sapiens.

XX W09634113-A2.
XX
XX 11-OCT-1996.
XX
XX 24-APR-1996; 9600-0505069
XX
XX 27-APR 1996; 9600-0400664.
XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX Brown MS, Goldstein JL, James GL;
XX
XX WFI; 1996-047642/49.
XX
XX Assay for farnesyl transferase activity - by determining ability to
XX transfer farnesyl moiety to K-ras B protein, partic. useful for
XX identifying inhibitors
XX
XX Example 5; Page 213-215, 257pp; English.
XX
XX AAW04473 is one isoform of the human K-ras B protein. The human
XX K-ras B enzyme is alternatively spliced and the translated protein
XX may include one of two different even tyrosine. The K-ras B protein
XX was used in a method for identifying phenyl transferase inhibitors.
XX The method involves screening candidate compounds for the ability to
XX inhibit the transfer of a farnesyl (four-carbon) isoprenoid moiety
XX to a K-ras B protein. Inhibitors act by blocking the attachment
XX of farnesyl groups to the proteins in malignant cells. A farnesyl
XX isoprenoid is a lipid molecule in pre-neoplastic states, and as such are used
XX to treat such conditions
XX
XX Sequence 188 AA;

Query Match 100.0%, Score 20; DB 17; Length 188;
Best Local Similarity 100.0%; Prod No. 0.0047;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPGQYKYYKYYKYYK 14
D6 171 SPGQYKYYKYYKYYK 184

Search completed: March 3, 2003, 06:18:45
Total time: 07:06:03 secs


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; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 00/081,496
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 00/178,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 00/146,735
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 00/187,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 00/196,133
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 89
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-056-89

Query Match      85.7%; Score 60; DR 10; Length 18;
Best Local Similarity 100.0%; Pred No. 0.012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPDKKFFKSK 12
   |||||
Db 7 SPDKKFFKSK 18

RESULT 3
US-09-984-057-89
; Sequence 89, Application US/09984057
; Patent No. US6003015/1677A1
; GENERAL INFORMATION:
; APPLICANT: BOGUCH, SAMUEL
; TITLE OF INVENTION: FEELINGS AND METHODS OF IDENTIFYING
; FILE REFERENCE: 0945-249
; CURRENT APPLICATION NUMBER: 08/00984,057
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/163,130
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 00/178,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 00/146,735
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 00/187,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 00/196,133
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 89
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-057-89

Query Match      85.7%; Score 60; DR 10; Length 18;
Best Local Similarity 100.0%; Pred No. 0.012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPDKKFFKSK 12
   |||||
Db 7 SPDKKFFKSK 18

RESULT 4
US-09-945-249-84
; Sequence 84, Application US/09045249
; Patent No. US6002001/0184A1
; GENERAL INFORMATION:
; APPLICANT: BERLIN, VIVIAN

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; APPLICANT: DANACHEZ, VERONIQUE
; APPLICANT: SMITH, SIOBHAN E
; TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING ANTI-PITUITARY AGENTS,
; TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING ANTI-PITUITARY AGENTS,
; FILE REFERENCE: MIV-074-06
; CURRENT APPLICATION NUMBER: 09/09045,249
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 00/041,950
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: 00/077,212
; PRIOR FILING DATE: 1996-12-20
; PRIOR APPLICATION NUMBER: 08/631,419
; PRIOR FILING DATE: 1996-04-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Participation of Artificial Sequence: Peptide that
; OTHER INFORMATION: corresponds to the C-terminal of protein of interest
; OTHER INFORMATION: substrates
US-09-945-249-84

Query Match      78.6%; Score 55; DR 9; Length 15;
Best Local Similarity 100.0%; Pred No. 0.049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GPKKFFKSK 14
   |||||
Db 1 GPKKFFKSK 11

RESULT 5
US-09-784-819-2
; Sequence 2, Application US/00784818
; Publication No. US6000102/83A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Eisenberg, Christopher J.
; APPLICANT: Bergman, Jeffrey M.
; TITLE OF INVENTION: PEPTIDE PROTEIN TRANSFERASE INHIBITORS
; FILE REFERENCE: 20496
; CURRENT APPLICATION NUMBER: 00/0784,818
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 00/183,451
; PRIOR FILING DATE: 2000-02-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthesized sequence
US-09-784-819-2

Query Match      78.6%; Score 55; DR 9; Length 15;
Best Local Similarity 100.0%; Pred No. 0.049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GPKKFFKSK 14
   |||||
Db 1 GPKKFFKSK 11

RESULT 6
US-09-970-967-2
; Sequence 2, Application US/00970967
; Patent No. US6002001/0184A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.

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us-09-214-913-41.rapb

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100.0%; Score 55; DB 10; Length 15;
 100.0%; Pred. No. 0.049;
 0; Mismatches 0; Indels 0; Gaps 0;

100.0%; Score 55; DB 10; Length 15;
 100.0%; Pred. No. 0.049;
 0; Mismatches 0; Indels 0; Gaps 0;

100.0%; Score 55; DB 10; Length 15;
 100.0%; Pred. No. 0.049;
 0; Mismatches 0; Indels 0; Gaps 0;

100.0%; Score 55; DB 10; Length 15;
 100.0%; Pred. No. 0.049;
 0; Mismatches 0; Indels 0; Gaps 0;

US/0919522

100.0%; Score 55; DB 10; Length 15;
 100.0%; Pred. No. 0.049;
 0; Mismatches 0; Indels 0; Gaps 0;

100.0%; Score 55; DB 10; Length 15;
 100.0%; Pred. No. 0.049;
 0; Mismatches 0; Indels 0; Gaps 0;

100.0%; Score 55; DB 10; Length 15;
 100.0%; Pred. No. 0.049;
 0; Mismatches 0; Indels 0; Gaps 0;

100.0%; Score 55; DB 10; Length 15;
 100.0%; Pred. No. 0.049;
 0; Mismatches 0; Indels 0; Gaps 0;

100.0%; Score 55; DB 10; Length 15;
 100.0%; Pred. No. 0.049;
 0; Mismatches 0; Indels 0; Gaps 0;

100.0%; Score 55; DB 10; Length 15;
 100.0%; Pred. No. 0.049;
 0; Mismatches 0; Indels 0; Gaps 0;

100.0%; Score 55; DB 10; Length 15;
 100.0%; Pred. No. 0.049;
 0; Mismatches 0; Indels 0; Gaps 0;

100.0%; Score 55; DB 10; Length 15;
 100.0%; Pred. No. 0.049;
 0; Mismatches 0; Indels 0; Gaps 0;

```

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Completely synthetic sequence
US-09-784-897A-2

Query Match          78.6%, Score 55, DB 10, Length 15;
Best Local Similarity 100.0%, Pred. No. 0.049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYFFVYKSTK 14
DB 1 GYFFVYKSTK 11

RESULT 11
US-09-770-983-2
Sequence 2, Application US/09770983
Patent No. US6000000A1
GENERAL INFORMATION:
APPLICANT: Merck & Co., Inc.
APPLICANT: Bergman, Christopher G.
APPLICANT: Bergman, Jeffrey M.
TITLE OF INVENTION: INHIBITORS OF PRENYL PROTEIN TRANSFERASE
FILE REFERENCE: 200309
CURRENT APPLICATION NUMBER US/09/770-983
PRIORITY FILING DATE: 2001-01-17
PRIORITY FILING DATE: 2003-01-17
PRIORITY FILING DATE: 2003-01-17
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 15
TYPE: PRT
ORGANISM: Homosapien
US-09-770-983-2

Query Match          78.6%, Score 55, DB 10, Length 15;
Best Local Similarity 100.0%, Pred. No. 0.049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYFFVYKSTK 14
DB 1 GYFFVYKSTK 11

RESULT 12
US-09-828-325A-3
Sequence 3, Application US/09828325A
Patent No. US6000000A1
GENERAL INFORMATION:
APPLICANT: Merck & Co., Inc.
APPLICANT: Craig A. Stump
APPLICANT: Theresa M. Williams
TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
FILE REFERENCE: 206367
CURRENT APPLICATION NUMBER US/09/828-325A
PRIORITY FILING DATE: 2001-08-17
PRIORITY FILING DATE: 2003-04-10
PRIORITY FILING DATE: 2003-04-10
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Completely Synthetic Amino Acid
US-09-828-325A-3

Query Match          78.6%, Score 55, DB 10, Length 15;
Best Local Similarity 100.0%, Pred. No. 0.049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 GYFFVYKSTK 14
DB 1 GYFFVYKSTK 11

RESULT 13
US-09-757-217A-3
Sequence 3, Application US/09757217A
Patent No. US6000000A1
GENERAL INFORMATION:
APPLICANT: Merck & Co., Inc.
APPLICANT: S. Jane deSolms
APPLICANT: Gerald E. Stokker
APPLICANT: Anthony W. Shaw
TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
FILE REFERENCE: 206037
CURRENT APPLICATION NUMBER US/09/757-217A
PRIORITY FILING DATE: 2001-06-25
PRIORITY FILING DATE: 2003-01-12
PRIORITY FILING DATE: 2003-01-12
NUMBER OF SEQ ID NOS: 75
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Completely Synthetic Amino Acid
US-09-757-217A-3

Query Match          78.6%, Score 55, DB 10, Length 15;
Best Local Similarity 100.0%, Pred. No. 0.049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYFFVYKSTK 14
DB 1 GYFFVYKSTK 11

RESULT 14
US-09-828-259A-3
Sequence 3, Application US/09828259A
Patent No. US6000000A1
GENERAL INFORMATION:
APPLICANT: Merck & Co., Inc.
APPLICANT: Diem N. Nguyen
APPLICANT: Craig A. Stump
APPLICANT: Theresa M. Williams
TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
FILE REFERENCE: 206377
CURRENT APPLICATION NUMBER US/09/828-259A
PRIORITY FILING DATE: 2001-04-09
PRIORITY FILING DATE: 2003-04-10
PRIORITY FILING DATE: 2003-04-10
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Completely Synthetic Amino Acid
US-09-828-259A-3

Query Match          78.6%, Score 55, DB 10, Length 15;
Best Local Similarity 100.0%, Pred. No. 0.049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYFFVYKSTK 14
DB 1 GYFFVYKSTK 11

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RESULT 2
US 08 564 164A 9
Sequence 9, Application US/08044164A
Patent No. 6100947
GENERAL INFORMATION:
APPLICANT: Schwaighoffer, Fabien
APPLICANT: Tocque, Bruno
TITLE OF INVENTION: Intracellular binding proteins and use
TITLE OF INVENTION: Title of
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Elanco Foodcare R&D Int.
STREET: 500 Arcola Road, 3643
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426 0107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/564,164A
FILING DATE: 28-DEC-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR94/00714
FILING DATE: 19-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 24,3741
FILING DATE: 16-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Cavitzky, Martin F.
REGISTRATION NUMBER: 33,699
REFERENCE/DOCKET NUMBER: ST02030 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)454-3816
TELEFAX: (610)454 3898
INFORMATION FOR SEQ ID NO. 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-564-164A-9
Query Match: 100%, Query ID: 184, Length: 24
Best Local Similarity: 100%, Prod No: 0.00000, Mismatches: 0, Indels: 0, Gaps: 0
Matches: 14, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0
CY 1 SYDGGKFFKFFKFFK 14
DB 7 SYDGGKFFKFFKFFK 20
RESULT 3
US 08 564 164A 9
Sequence 6, Application US/08044164A
Patent No. 6100947
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Method for the detection of E. coli antigens.
TITLE OF INVENTION: In particular the E. coli antigen
NUMBER OF SEQUENCES: 16
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EP)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/564,164A

1 FILING DATE: 1995, Query ID: 184, Length: 24
2 INFORMATION FOR SEQ ID NO: 6:
3 SEQUENCE CHARACTERISTICS:
4 LENGTH: 18 amino acids
5 TYPE: amino acid
6 STRANDEDNESS:
7 TOPOLOGY: linear
8 MOLECULE TYPE: peptide
9 US 08 564-329-5
Query Match: 100%, Query ID: 184, Length: 18
Best Local Similarity: 100%, Prod No: 0.0012, Mismatches: 0, Indels: 0, Gaps: 0
Matches: 14, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0
CY 1 SYDGGKFFKFFKFFK 14
DB 21 SYDGGKFFKFFKFFK 34
RESULT 4
US 08 429-964-34
Sequence 94, Application US/08429964
Patent No. 5302243
GENERAL INFORMATION:
APPLICANT: BROWN, MICHAEL S.
APPLICANT: GOLDSTEIN, JOSEPH L.
APPLICANT: REISS, YUVAL
APPLICANT: JAMES, GUY L.
TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF PARNESYL
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNO, WHITE & DRYER
STREET: P O BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,964
FILING DATE: 27-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/271,406
FILING DATE: 16-FEB-1993
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/922,611
FILING DATE: APPOINTED
CLASSIFICATION: 435
APPLICATION NUMBER: 187406/110240
FILING DATE: 18-APR-1991
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/615,715
FILING DATE: 20-NOV-1990
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/410,706
FILING DATE: 19-APR-1990 (ABANDONED)
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: USPT-417/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 418-3000
TELEFAX: (713) 781-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:

1 FILING DATE: 22 OCT-1987
2 APPLICATION NUMBER: 913,405
3 FILING DATE: 01-OCT-1986
4 APPLICATION NUMBER: 696,187
5 FILING DATE: 29 JAN-1985
6 SEQ ID NO: 17
7 LENGTH: 16
8 5443956-17

Query Match. 79.4%, Score 55, DP 0, Length 16,
Best Local Similarity 100.0%, Prod No. 0.062,
Matches 13; Conservative 6, Mismatches 0, Indels 0, Gaps 0

QV 1 SEGYHYHYFST 13
DB 4 SEGYHYHYFST 16

RESULT 8
US-08-985-337A-1
Sequence 1, Application US/08985337A
Patent No. 5932590
GENERAL INFORMATION:
APPLICANT: Ciccarone, Terrence M.
APPLICANT: deSolms, S. Jane
TITLE OF INVENTION: INHIBITORS OF FARNESYL PROTEIN
NUMBER OF INVENTION: TRANSFERASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 120 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,337A
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,578
FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 19814Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3903
TELEFAX: 908-594-4720
TELEX:

INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-985-337A-1

Query Match. 79.4%, Score 55, DP 0, Length 16,
Best Local Similarity 100.0%, Prod No. 0.062,
Matches 13; Conservative 6, Mismatches 0, Indels 0, Gaps 0

QV 4 GYHYHYHYFST 14
DB 1 GYHYHYHYFST 11

RESULT 9

US-08-985-124A-1
Sequence 1, Application US/08985124A
Patent No. 5972966
GENERAL INFORMATION:
APPLICANT: deSolms, S. Jane
TITLE OF INVENTION: INHIBITORS OF FARNESYL PROTEIN
NUMBER OF INVENTION: TRANSFERASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 120 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,124A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,428
FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 19813Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3903
TELEFAX: 908-594-4720
TELEX:

INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-985-124A-1

Query Match. 79.4%, Score 55, DP 2, Length 15,
Best Local Similarity 100.0%, Prod No. 0.062,
Matches 11; Conservative 0, Mismatches 0, Indels 0, Gaps 0

QV 4 GYHYHYHYFST 14
DB 1 GYHYHYHYFST 11

RESULT 10

US-08-985-320A-1
Sequence 1, Application US/08985320A
Patent No. 5977134
GENERAL INFORMATION:
APPLICANT: Ciccarone, Terrence M.
APPLICANT: Halczenko, Wasyl
APPLICANT: Hutchinson, John H.
APPLICANT: Lumma, Jr., William C.
APPLICANT: Stokker, Gerald E.
APPLICANT: Stump, Craig A.
APPLICANT: Williams, Theresa M.
TITLE OF INVENTION: INHIBITORS OF FARNESYL PROTEIN
NUMBER OF INVENTION: TRANSFERASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 120 E. Lincoln Ave.
CITY: Rahway

US-09-214-913-41.rai

Query Match 78.6%; Score 55; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 4 GKKKKKKSKTK 14
DB 1 GKKKKKKSKTK 11

RESULT 12
US-09-195-578-13
; Sequence 13, Application US/09195578
; Patent No. 6054466
; GENERAL INFORMATION:
; APPLICANT: Ciccarone, Terrence M.
; APPLICANT: desolms, Jane S. J.
; APPLICANT: Merck & Co., Inc.
; TITLE OF INVENTION: INHIBITORS OF FARNESYL-PROTEIN
; FILE REFERENCE: 20121Y
; CURRENT FILING DATE: 1998-11-18
; EARLIER FILING DATE: 1997-12-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homosapien
US-09-195-578-13

Query Match 78.6%; Score 55; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 4 GKKKKKKSKTK 14
DB 1 GKKKKKKSKTK 11

RESULT 13
US-09-140-557-13
; Sequence 13, Application US/09140557A
; Patent No. 6103487
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Barnett, Stanley F.
; APPLICANT: Heimbrock, David C.
; APPLICANT: Huber, Hans E.
; APPLICANT: Patrick, Denis R.
; TITLE OF INVENTION: A METHOD OF TREATING CANCER
; FILE REFERENCE: 20034Y
; CURRENT FILING DATE: 1998-08-26
; EARLIER FILING DATE: 1997-09-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0

US-09-214-913-41.rai

Query Match 78.6%; Score 55; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 4 GKKKKKKSKTK 14
DB 1 GKKKKKKSKTK 11

RESULT 12
US-09-195-578-13
; Sequence 13, Application US/09195578
; Patent No. 6054466
; GENERAL INFORMATION:
; APPLICANT: Ciccarone, Terrence M.
; APPLICANT: desolms, Jane S. J.
; APPLICANT: Merck & Co., Inc.
; TITLE OF INVENTION: INHIBITORS OF FARNESYL-PROTEIN
; FILE REFERENCE: 20121Y
; CURRENT FILING DATE: 1998-11-18
; EARLIER FILING DATE: 1997-12-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homosapien
US-09-195-578-13

Query Match 78.6%; Score 55; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 4 GKKKKKKSKTK 14
DB 1 GKKKKKKSKTK 11

RESULT 13
US-09-140-557-13
; Sequence 13, Application US/09140557A
; Patent No. 6103487
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Barnett, Stanley F.
; APPLICANT: Heimbrock, David C.
; APPLICANT: Huber, Hans E.
; APPLICANT: Patrick, Denis R.
; TITLE OF INVENTION: A METHOD OF TREATING CANCER
; FILE REFERENCE: 20034Y
; CURRENT FILING DATE: 1998-08-26
; EARLIER FILING DATE: 1997-09-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 12
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthesized peptide substrate for
; OTHER INFORMATION: Geranylgeranyl:protein transferase type I
US-09-164-482-13

; OTHER INFORMATION: synthesized peptide substrate for
; OTHER INFORMATION: Geranylgeranyl:protein transferase type I
US-09-140-557-13

Query Match 78.6%; Score 55; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GPKKKKKSKTK 14
| | | | | | | | | | | | | | | | |
DB 1 GPKKKKKSKTK 11

RESULT 14

US-09-170-951-13
; Sequence 13, Application US/09164482A
; Patent No. 6103723
; GENERAL INFORMATION:
; APPLICANT: Bergman, Jeffrey M.
; APPLICANT: Dinsmore, Christopher J.
; APPLICANT: Graham, Samuel L.
; APPLICANT: Merck & Co. Inc.
; TITLE OF INVENTION: INHIBITORS OF FARNESYL PROTEIN
; TITLE OF INVENTION: TRANSFERASE
; FILE REFERENCE: 19867Y
; CURRENT APPLICATION NUMBER: US/09/170,951
; CURRENT FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 60/064,343
; EARLIER FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homosapien
US-09-170-951-13

Query Match 78.6%; Score 55; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GPKKKKKSKTK 14
| | | | | | | | | | | | | | | | |
DB 1 GPKKKKKSKTK 11

RESULT 15

US-09-164-482-13
; Sequence 13, Application US/09164482A
; Patent No. 6127390
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: deSolms, S. Jane
; APPLICANT: Luma, William C.
; APPLICANT: Shaw, Anthony W.
; APPLICANT: Sisko, John T.
; APPLICANT: Tucker, Thomas J.
; TITLE OF INVENTION: INHIBITORS OF FARNYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20025Y
; CURRENT APPLICATION NUMBER: US/09/164,482A
; CURRENT FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: 60/060,871
; EARLIER FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: synthesized peptide substrate for
; OTHER INFORMATION: Geranylgeranyl:protein transferase type I
US-09-164-482-13

Query Match 79.6%; Score 55; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GPKKKKKSKTK 14
| | | | | | | | | | | | | | | | |
DB 1 GPKKKKKSKTK 11

Search completed: March 3, 2003, 06:15:52
Job time: 10.878 secs


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RESULT 11
H64008
C:Species: Haemophilus influenzae strain Rd PW-0
C:Date: 18-Aug-1995 #sequence_revision 19-Aug-1995 #text_update 30-Jun-1996
C:Accession: H64008
R:Flaichmann, E.D.; Adams, W.D.; White, C.; Clayton, E.A.; Finkbeiner, E.R.; Fierman, J.; Gagey, J.D.; Scott, J.J.; Shirley, P.; Liu, L.H.; Glaser, A.; Bailey, J.M.; Weinman, D.M.; Brandon, R.C.; Pine, L.D.; Pittman, U.L.; Finkbeiner, S.; Gershon, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, J.M.; Smith, H.A.; Gordon, A.L.
Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd
A:Reference number: A64008; MIM:604470; PMID:754180
A:Accession: H64008
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-14 <IG>
A:Cross-references: GB:022731; GB:044224; MIM:604470; PMID:754180
Query March 25.3% Score 119 PB 24 Length 147
Best Local Similarity 50.0% Pred. 53.6a 0.1
Matches 50 Conservative

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RESULT 12
PL0040
glycogen phosphorylase EC 2.4.1.1, cardiac - pig stomach
C.Species Sus scrofa domestica pig.
C.Date: 30-Jun-1992 #sequence_revision 1, Jun 1992 date added 11 May 2006
C.Accession: FJ0040
R.Dombrowski, V.J.Willis, A.C. Vereb, J.L. Johnson, L.N.
Comp. Biochem. Physiol. B 91, 71-72, 1984
A.Title: the sequence around the phosphorylation site of the porcine heart type I glycogen
A.Reference number: PL0040; M01D8916357; P010121547
A.Accession: E10040
A.Molecule type: protein
A.Pesidues: 1-14 <DOM>
A.Experimental source: heart
C.Keywords: allosteric regulation; cardiac muscle; glycogen metabolism; glycosylation
E.F.I/CBinding site, phosphate 3001, 3002, 3003, 3004, 3005, 3006, 3007, 3008, 3009, 3010, 3011, 3012, 3013, 3014, 3015, 3016, 3017, 3018, 3019, 3020, 3021, 3022, 3023, 3024, 3025, 3026, 3027, 3028, 3029, 3030, 3031, 3032, 3033, 3034, 3035, 3036, 3037, 3038, 3039, 3040, 3041, 3042, 3043, 3044, 3045, 3046, 3047, 3048, 3049, 3050, 3051, 3052, 3053, 3054, 3055, 3056, 3057, 3058, 3059, 3060, 3061, 3062, 3063, 3064, 3065, 3066, 3067, 3068, 3069, 3070, 3071, 3072, 3073, 3074, 3075, 3076, 3077, 3078, 3079, 3080, 3081, 3082, 3083, 3084, 3085, 3086, 3087, 3088, 3089, 3090, 3091, 3092, 3093, 3094, 3095, 3096, 3097, 3098, 3099, 3100, 3101, 3102, 3103, 3104, 3105, 3106, 3107, 3108, 3109, 3110, 3111, 3112, 3113, 3114, 3115, 3116, 3117, 3118, 3119, 3120, 3121, 3122, 3123, 3124, 3125, 3126, 3127, 3128, 3129, 3130, 3131, 3132, 3133, 3134, 3135, 3136, 3137, 3138, 3139, 3140, 3141, 3142, 3143, 3144, 3145, 3146, 3147, 3148, 3149, 3150, 3151, 3152, 3153, 3154, 3155, 3156, 3157, 3158, 3159, 3160, 3161, 3162, 3163, 3164, 3165, 3166, 3167, 3168, 3169, 3170, 3171, 3172, 3173, 3174, 3175, 3176, 3177, 3178, 3179, 3180, 3181, 3182, 3183, 3184, 3185, 3186, 3187, 3188, 3189, 3190, 3191, 3192, 3193, 3194, 3195, 3196, 3197, 3198, 3199, 3200, 3201, 3202, 3203, 3204, 3205, 3206, 3207, 3208, 3209, 3210, 3211, 3212, 3213, 3214, 3215, 3216, 3217, 3218, 3219, 3220, 3221, 3222, 3223, 3224, 3225, 3226, 3227, 3228, 3229, 3230, 3231, 3232, 3233, 3234, 3235, 3236, 3237, 3238, 3239, 3240, 3241, 3242, 3243, 3244, 3245, 3246, 3247, 3248, 3249, 3250, 3251, 3252, 3253, 3254, 3255, 3256, 3257, 3258, 3259, 3260, 3261, 3262, 3263, 3264, 3265, 3266, 3267, 3268, 3269, 3270, 3271, 3272, 3273, 3274, 3275, 3276, 3277, 3278, 3279, 3280, 3281, 3282, 3283, 3284, 3285, 3286, 3287, 3288, 3289, 3290, 3291, 3292, 3293, 3294, 3295, 3296, 3297, 3298, 3299, 3300, 3301, 3302, 3303, 3304, 3305, 3306, 3307, 3308, 3309, 3310, 3311, 3312, 3313, 3314, 3315, 3316, 3317, 3318, 3319, 3320, 3321, 3322, 3323, 3324, 3325, 3326, 3327, 3328, 3329, 3330, 3331, 3332, 3333, 3334, 3335, 3336, 3337, 3338, 3339, 3340, 3341, 3342, 3343, 3344, 3345, 3346, 3347, 3348, 3349, 3350, 3351, 3352, 3353, 3354, 3355, 3356, 3357, 3358, 3359, 3360, 3361, 3362, 3363, 3364, 3365, 3366, 3367, 3368, 3369, 3370, 3371, 3372, 3373, 3374, 3375, 3376, 3377, 3378, 3379, 3380, 3381, 3382, 3383, 3384, 3385, 3386, 3387, 3388, 3389, 3390, 3391, 3392, 3393, 3394, 3395, 3396, 3397, 3398, 3399, 3400, 3401, 3402, 3403, 3404, 3405, 3406, 3407, 3408, 3409, 3410, 3411, 3412, 3413, 3414, 3415, 3416, 3417, 3418, 3419, 3420, 3421, 3422, 3423, 3424, 3425, 3426, 3427, 3428, 3429, 3430, 3431, 3432, 3433, 3434, 3435, 3436, 3437, 3438, 3439, 3440, 3441, 3442, 3443, 3444, 3445, 3446, 3447, 3448, 3449, 3450, 3451, 3452, 3453, 3454, 3455, 3456, 3457, 3458, 3459, 3460, 3461, 3462, 3463, 3464, 3465, 3466, 3467, 3468, 3469, 3470, 3471, 3472, 3473, 3474, 3475, 3476, 3477, 3478, 3479, 3480, 3481, 3482, 3483, 3484, 3485, 3486, 3487, 3488, 3489, 3490, 3491, 3492, 3493, 3494, 3495, 3496, 3497, 3498, 3499, 3500, 3501, 3502, 3503, 3504, 3505, 3506, 3507, 3508, 3509, 3510, 3511, 3512, 3513, 3514, 3515, 3516, 3517, 3518, 3519, 3520, 3521, 3522, 3523, 3524, 3525, 3526, 3527, 3528, 3529, 3530, 3531, 3532, 3533, 3534, 3535, 3536, 3537, 3538, 3539, 3540, 3541, 3542, 3543, 3544, 3545, 3546, 3547, 3548, 3549, 3550, 3551, 3552, 3553, 3554, 3555, 3556, 3557, 3558, 3559, 3560, 3561, 3562, 3563, 3564, 3565, 3566, 3567, 3568, 3569, 3570, 3571, 3572, 3573, 3574, 3575, 3576, 3577, 3578, 3579, 3580, 3581, 3582, 3583, 3584, 3585, 3586, 3587, 3588, 3589, 3590, 3591, 3592, 3593, 3594, 3595, 3596, 3597, 3598, 3599, 3600, 3601, 3602, 3603, 3604, 3605, 3606, 3607, 3608, 3609, 3610, 3611, 3612, 3613, 3614, 3615, 3616, 3617, 3618, 3619, 3620, 3621, 3622, 3623, 3624, 3625, 3626, 3627, 3628, 3629, 3630, 3631, 3632, 3633, 3634, 3635, 36

DB 2 DGERPKQ 8

RESULT 13

PN0118
hemoglobin beta chain - red fox (fragment)
C.Species: Vulpes vulpes (red fox) (fragment)
C.Create: 15-Jan-1993 #sequence revision 15-Jan-1993 #seq. dates: 19-May 1993
C.Accession: P0118
R.Sukhomlinov, B.F.; Konchevsky, S.V.
Mol. Biol. (Mosk.) 5, 415-418, 1971
A.Title: Study on N-terminal sequence of the haemoglobin of Vulpes vulpes fox.
A.Reference number: PN0117
A.Accession: PN0118
A.Molecule type: protein
A.Residues: 1-15 <SHK>
C.Superfamily: globin; globin homology
C.Keywords: blood, erythrocytes, hemoglobin, hemoglobin chain, erythron, erythrocytes

Query Match 25.3% Score 211 DP 2 Length 154
Best Local Similarity 41.1% Pred. NO. 6.4e-04
Matches 5; Conservative 1; Mismatches 6; Indels 1; Gaps 0

QY 5 KKKKSPKSG 16
 : : : :
 Db 4 KKKKSPKSG 15

RESULT 14

A27803
 myosin light chain, smooth muscle - turkey (fragment)
 C;Species: Meleagris gallopavo (common turkey)
 C;Date: 05-Jun-1998 #sequence_revision 65-Jun-1998 #text_change 29-Sep-1999
 C;Accession: A27803
 R;Receptor: A.R.; Robinson, E.A.; Appella, E.; Sellers, J.R.
 J. Biol. Chem. 262, 7613-7617, 1987
 A;Title: Sequence of the sites phosphorylated by protein kinase C in the smooth muscle m
 A;Reference number: A27803; PMID:9722380; PMID:3584131
 A;Accession: A27803
 A;Molecule type: protein
 A;Residues: 1-16 <R>
 C;Superfamily: calmodulin, calmodulin-regulat homology
 C;Keywords: EF hand; muscle; smooth muscle

Query Match 25.3%, Score 21, DB 2, Length 16;
 Best Local Similarity 44.4%, Pred. No. 6.7e+03;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 KKKKSPKSG 13
 : : : :
 Db 4 KKKKSPKSG 15

RESULT 15

PH0137
 T-cell receptor beta chain V-D-J region MS20 - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 21-Nov-1991 #sequence_revision 02-Nov-1991 #text_change 10-May-1997
 C;Accession: PH0137
 R;Receptor: F.; H-well, M.D.; Teraoka, H.; Fritzsche, M.; Rickett, J.; Bruchoff, S.; Lo
 J. Exp. Med. 173, 19-24, 1991
 A;Title: A myelin basic protein peptide is recognized by cytotoxic T cells in the contex
 A;Reference number: PH0137; PMID:5104543; PMID:1762137
 A;Accession: PH0137
 A;Molecule type: mRNA
 A;Residues: 1-16 <MAR>
 C;Keywords: T-cell receptor

Query Match 25.3%, Score 21, DB 2, Length 16;
 Best Local Similarity 66.7%, Pred. No. 6.7e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 KKKSPS 12
 : : : :
 Db 7 KKKSPS 12

Search completed: March 3, 2003, 06:46:26
 Job time : 14.6667 secs


```

GN RPSS OR RPS19.
OS Cloning and differentiation Phytoplasm.
OC Bacteria, Firmicutes, Mollicutes; Achleoplasmatales;
OC Achleoplasmatales; Phytoplasm.
OX NCBI_TaxID=35776;
RN [1]
RP SEQUENCE FROM N.A.
FX MEDLINE: 9450922; PubMed: 971198.
RA Gunderson D.E., Lee I.M., Rehner S.A., Davis P.E., Kingbury D.T.
RT "Phylogeny of mycoplasma-like organisms (phytoplasm): a basis for
PT their classification".
PL J. Bacteriol. 176:5244-5254(1994).
CC 1- PUNISHING: 176:5244-5254(1994).
CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC 1- SIMILARITY: BELONGS TO THE 16S FAMILY OF RIBOSOMAL PROTEINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@ebi.ac.uk.
CC
CC EMBL: L27027; AAA93944.1;
DE Bacteria, Firmicutes, Mollicutes, Achleoplasmatales;
DE PROSITE: PS00073; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein, rRNA-binding.
FT NON-TER 1
SQ SEQUENCE 14 AA; 1642 MW; 20C478EB0FFFE48 CRC64;

Query Match 31.93; Score 25; DB 1; Length 14;
Best local similarity 31.93; Pct Id 100.00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q/ 2 SPYVPPV 9
D/ 7 GDRNKK 14

RESULT 3
PS19 LOWEP
ID R13 LOWEP STANDARD; PRT; 14 AA.
AC Q48878;
DT 30-MAY-2000 (rel 30, last sequence update)
DT 30-MAY-2000 (rel 30, last annotation update)
DE 30S ribosomal protein S19 (fragment).
GN R13 LOWEP.
OS Loofah witches'-broom phytoplasm.
OC Bacteria, Firmicutes, Mollicutes, Achleoplasmatales;
OC Achleoplasmatales; Phytoplasm.
OX NCBI_TaxID=35776;
RN [1]
RP SEQUENCE FROM N.A.
FX MEDLINE: 9450922; PubMed: 971198.
RA Gunderson D.E., Lee I.M., Rehner S.A., Davis P.E., Kingbury D.T.
RT "Phylogeny of mycoplasma-like organisms (phytoplasm): a basis for
PT their classification".
PL J. Bacteriol. 176:5244-5254(1994).
CC 1- PUNISHING: 176:5244-5254(1994).
CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC 1- SIMILARITY: BELONGS TO THE 16S FAMILY OF RIBOSOMAL PROTEINS.
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CC or send an email to license@ebi.ac.uk.
CC
CC EMBL: L27027; AAA93944.1;
DE Bacteria, Firmicutes, Mollicutes, Achleoplasmatales;
DE PROSITE: PS00073; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein, rRNA-binding.
FT NON-TER 1
SQ SEQUENCE 14 AA; 1642 MW; 20C478EB0FFFE48 CRC64;

Query Match 28.93; Score 24; DB 1; Length 14;
Best local similarity 28.93; Pct Id 100.00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q/ 2 SPYVPPV 13
D/ 7 GDRNKK 14

RESULT 5
PS19 PRUAP
ID R519 PRUAP STANDARD; PRT; 14 AA.
AC Q44160;
DT 30-MAY-2000 (rel 30, last sequence update)
DT 30-MAY-2000 (rel 30, last annotation update)
DE 30S ribosomal protein S19 (fragment).
GN RPS19 OR RPS19.
OS Pinus albertiana phytoplasm.

```

SECRET

100

11	1	1	1
NON PER			
SEQUENCE	12 AA;	1263 MW;	2004-09-23 00:33:55

1978; Scher S.A., Davis R.M., Kingsley C.T.
These organisms have formed a basis for

Q. CDKXXXXX 9

[illegible]

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TAL TREPB

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CC C + 2 H2O/O
FW Oxidoreductase; Micro-oxidation
FT NON-TER 10 10
SQ SEQUENCE 10 AA; 1210 MW; 470587771A33322 QPCW4;

Query Match 24.1%, Score 20, DB 1, Length 10,
Best Local Similarity 50.0%, Field No. 17503,
Matches 3, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

CY - PPTPT 10
:|:|:|
DB 3 QKWTPT 8

RESULT 2
RPOC_MYCGA STANFORD, PPT, 13 AA;
ID RPOC_MYCGA STANFORD, PPT, 13 AA;
AC P4716;
DT 01-FEB-1996 (Rel 33, Created)
ET 01-FEB-1996 (Rel 33, Last sequence update)
DT 16-OCT-2000 (Rel 40, Last annotation update)
DE RNA directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase
DE beta' chain) (RNA polymerase beta' subunit) (Fragment)
GN RPOC;
OS Mycoplasma Gallisepticum
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma;
CY NCBI_TaxID=1074;
RN [1]_
SEQUENCE FROM N.A.
R STAFFAN AGGEVALL F.
PA Rebeccalashvili P S;
RA Rebeccalashvili P S;
RL Submitted (XXY 1000) to the EMBL/GenBank/CCP3 databases
CC 1- FUNCTION: RNA DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR PHOSPHORIBOSIDE TRIPHOSPHATES AS
CC SUBSTRATES
CC 1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA}(N)
CC 1- SUBMIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
CC BETA' CHAIN.
CC 1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: L39403; AAB40952.1; ...
FW Transcription: RNA-directed RNA polymerase, Transcription.
FT NON-TER 11 11
SQ SEQUENCE 13 AA; 1430 MW; 4P22777486C413 QP764;

Query Match 24.1%, Score 20, DB 1, Length 10,
Best Local Similarity 50.0%, Field No. 22603,
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

CY 1 PPTPTT 8
:|:|:|
DB 4 PPTPTT 11

RESULT 10
RS19_PPWPB STANFORD, PPT, 14 AA
ID RS19_PPWPB STANFORD, PPT, 14 AA
AC Q22002;
DT 30-MAY-2000 (Rel 39, Last sequence update)
DT 30-MAY-2000 (Rel 39, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).

```



```

AC P12509;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE TAT protein (Transactivating regulatory protein) (Fragment)
GN TAT
OS Human immunodeficiency virus type 1 (HIV-1 isolate) (HIV-1).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI TaxID:11795;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE 8619450; PubMed 3511779;
RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.B., Markham P.D.,
RA Gallo R.C., Weng S.F., Gallo R.C., Parks E.S., Parks W.F.,
RA Genetic variation in HIV-1/HIV-2 over time in patients with AIDS or
RT at risk for AIDS."
RL Sequence 214-913-37 (1996).
CC : FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE TAR
CC PROMOTER.
CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nucleolus, Nucleolus.
CC -!- MISCELLANEOUS: LOCATES WNT1, WNT2, AND WNT3 WERE OBTAINED FROM
CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO YEAR OLD HAITIAN WHO
CC WAS PERINATALLY INFECTED BY HER MOTHER.
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CC
CC EMBL: M12507; AAB12991.1;
CC HIV; M12507; TATSWM02.
CC Transcription regulation, Activation, RNA-binding, Nuclear protein;
CC AIDS.
KW AIDS
FT NON_TER 1 1
SQ SEQUENCE 14 AA: 146/ MW: 37007378F8F67AA8 CRC64;
Query Match 22.9%; Score 19; DB 1; Length 14;
Best Local Similarity 75.0%; Pred. NO. 3.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 GPKK 5
DB 11 GPKK 14
RESULT 15
TAT_HV128
ID TAT_HV128 STANDARD; PRT; 14 AA.
AC P12511;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE TAT protein (Transactivating regulatory protein) (Fragment).
GN TAT.
OS Human immunodeficiency virus type 1 (294 isolate) (HIV-1).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI TaxID:11681;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE 98281278; PubMed 3395517;
RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.B., Markham P.D.,
RA Gallo R.C.,
RA Genetic variation in HIV-1/HIV-2 over time in patients with AIDS or
RT at risk for AIDS."
RL Sequence 214-913-37 (1996).
CC : FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE TAR
CC PROMOTER.
CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nucleolus, Nucleolus.
CC -!- MISCELLANEOUS: LOCATES WNT1, WNT2, AND WNT3 WERE OBTAINED FROM
CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO YEAR OLD HAITIAN WHO
CC WAS PERINATALLY INFECTED BY HER MOTHER.
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CC
CC EMBL: J03653; AAA44685.1;
CC HIV; J03653; TATSWM1.
CC Transcription regulation, Activation, RNA-binding, Nuclear protein;
CC AIDS.
KW AIDS
FT NON_TER 1 1
SQ SEQUENCE 14 AA: 1453/ MW: 37007378F8F67AA8 CRC64;
Query Match 22.9%; Score 19; DB 1; Length 14;
Best Local Similarity 75.0%; Pred. NO. 3.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 GPKK 5
DB 11 GPKK 14
Search completed March 3, 2003, 06:42:07
File: 214-913-37

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DT	C1 MAR 2001	(TRENBERG) 16, Cited)
DT	01-MAR-2001	(TEMPERED) 16, last sequence update)
DT	01-MAR-2001	(TEMPERED) 16, last annotation update)
DE	P53	tumor suppressor (Fragment).
DE	P53.	
GN		
OS	Rattus norvegicus (Rat).	
OS	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;	
CC	NCBI_TaxID=10116,	
CC	"11_TaxID=10116,"	
FN		
FP	SEQUENCE FROM N.A.	
RP		
FW	16 W 16, H816 W 16	
FA	16 W 16, H816 W 16	
FL	Submitted (Aug-2001) to the EMBL/GenBank/DDBJ databases	
PL	EMBL; AF274447, AA924167.	
OR	NON TER	1
FT	NON TER	16
FT	NON TER	16
SO	SEQUENCE	16 AA: 1991 MW: 19919051454152 19914:

Q7 PPTKFFKFSPOV 12
 : : : : :
 Db PPTKFGOSTSR 12

RESULT 3

092PB8	Q54PB5	PRELIMINARY	EFF	14 AA
ID	Q99PB8			
DT	01-JUN 2001 (TEMPREL 17, Created)			
DT	01-JUN 2001 (TEMPREL 17, Last sequence update)			
DT	01-JUN 2001 (TEMPREL 17, Last annotation update)			
DE	Adenosine kinase (EC 2.7.1.20) (Fragment).			
DE	Xes musculus (Muscle).			
CC	Eukaryota; Metazoa; Chordata; Chordata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Scuriomyrini; Muridae; Murinae; Mus;			
CC	NCBI_Taxid=10090;			
CC	111			
PP	SEQUENCE FROM N.A.			
RA	Singh R, Lin A, Wu Z, Gupta P S			
RT	"Gene Structure for Adenosine Kinase in Chinese Hamster and Human:			
RT	High Frequency Mutants of CHO Cells Involve Deletions of several			
RT	Intons and exons."			
RT	DNA Cell Biol.			
RL	EMBL; AF318953; AA071861;			
FW	Kinase; transase.			
FT	NON TER			
FT	14			
FT	SEQUENCE 14 AA; 156 MW.			

2y 1 DGPKKKK 9
| | | | |
3b 5 DEPKPKKK 13

RESULT 4

[illegible]

NCBI TaxID:2155;
[1]
RN
PP SEQUENCE FROM N.A.
RA Lim P.O., Sears B.B.;
RNA DNA sequence of the ribosomal protein genes rp12 and rp19 from a
RPT plant pathogenic mycoplasma-like organism.";
RFL FEMS Microbiol. Lett. 61:71-74(1991).
EN [2]
RN
PP SEQUENCE FROM N.A.
EX WEINSTEIN M., SCHARF R.M., LITVINSON,
RA Lim P.O., Sears B.B.;
RNA Evolutionary relationships of a plant pathogenic mycoplasma-like
organism and A. Mycoplasma laidlawii isolated from a wheat ribosomal protein
gene sequences;
RFL Sears B.B., Lim P.O. J Mol Biol 180(1992).
DR EMBL; M74770; AAA25331; 17
EN 14
PP NON TER
SEQUENCE IN AA: 1470 MW: 27230;PIR:AAA251 CR664;

2	PRFRFRFRSSK	13
		:
4	PKFTKYPFRPH	14

RESULT 5

Q84271 PRELIMINARY; PRT; 8 AA.
 AC Q84271; 1986 (TEMPORAL 01, Created)
 DT 01-NOV-1986 (TEMPORAL 01, Last sequence update)
 DT 01-NOV-1986 (TEMPORAL 08, Last annotation update)
 DE LI protein (Fragment).
 OS Human Papillomavirus type 19.
 OC Viruses; DNA viruses; DNA RNA virus; Papillomaviridae;
 OC Papillomavirus
 NCBI_taxid=10608;
 RN [1]
 RF SEQUENCE FROM N.A.
 RP MFMUINR8809511; PubMed=2826651;
 RA Kribe J., Kraus J., Fellus H., Chow T., Proker T.R., Iffert T.,
 RA Pfister H.;
 RT "Genetic relationship among human papillomaviruses associated with
 RT benign and malignant lesions of the cervix with epitheliomylasia
 RT verruciformis";
 RT J Gen Virol 69:2091-2103(1987).
 DE EM21; D00104; EAA00142.1 -;
 FT NON TER 1 1
 FT SEQUENCE 8 AA; 197 MW; 1E442401246121A8; SEC64;

	MATCHES	4	(C)
Qy	2	SPKPKKK	8
Dp	1	GTRPRRK	7

RESULTS

[illegible]

Query Match 28.9% Score 24; DB 2; Length 14;
Best Local Similarity 66.7% Pred. No. 2, Gaps 0;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QV 1 DGPXK 6
DB 4 DGPXK 9
RESULT 9
QNZH9 PRELIMINARY; PRT; 16 AA.
AC QNZH9
DI 01-OCT-2000 (TrEMBLrel. 15, Created)
DI 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DI 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Fibroblast growth factor homologous factor 2 isoform 1 only
DE (Fragment).
GN FHF-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2012823; PubMed=1064718;
RA Muncz Sanjuan I.; Smallwood P.M.; Nathans J.;
RT "Isoform diversity among fibroblast growth factor homologous factors
RT Is Generated by Alternative Promoter Usage and Differential
RT Splicing".
EL J Biol Chem. 275:2599-2597(2000).
DR EMBL; AF199613; AAF31403.1;
FT NON TER 16
SQ SEQUENCE 16 AA; 1763 MW; 70D5A3075CE769; CD064;
Query Match 28.9% Score 24; DB 4; Length 14;
Best Local Similarity 50.0% Pred. No. 3, Gaps 0;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QV 4 YWYVYSPK 13
DB 7 YWYVYSPK 16
RESULT 10
Q94623 PRELIMINARY; PRT; 8 AA.
AC Q94623
DI 01-FEB-1997 (TrEMBLrel. 02, Created)
DI 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DI 01-NOV-1998 (TrEMBLrel. 04, Last annotation update)
DE MSUSP-2 protein (Fragment).
GN USP.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Lepidoptera;
OC Preytorata; Neoptera; Endopterygota; Lepidoptera; Tortricidae;
OC Spingidae; Spingidae; Spingidae; Manduca.
OX NCBI_TaxID 7130;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EPIDERMIS;
RX MEDLINE=97165493; PubMed=903254;
RA Jindra M.; Huang J.Y.; Malone F.; Asahina M.; Radford J.M.;
RT "Identification and mRNA developmental profiles of two alternative
RT isoforms in the epidermis and wings of Manduca sexta".
RL Insect Mol. Biol. 6:41-53(1997).
DR EMBL; U5902; AAB64235.1;
FT NON TER 8
SQ SEQUENCE 8 AA; 892 MW; F155B5415A75B1; CD564;
Query Match 27.7% Score 23; DB 5; Length 14;
Best Local Similarity 66.7% Pred. No. 6, Gaps 0;

Query Match 28.9% Score 24; DB 2; Length 14;
Best Local Similarity 66.7% Pred. No. 2, Gaps 0;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QV 1 DGPXK 6
DB 4 DGPXK 9
RESULT 9
QNZH9 PRELIMINARY; PRT; 14 AA.
AC QNZH9
DI 01-OCT-2000 (TrEMBLrel. 15, Created)
DI 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DI 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Fibroblast growth factor homologous factor 2 isoform 1 only
DE (Fragment).
GN FHF-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2012823; PubMed=1064718;
RA Muncz Sanjuan I.; Smallwood P.M.; Nathans J.;
RT "Isoform diversity among fibroblast growth factor homologous factors
RT Is Generated by Alternative Promoter Usage and Differential
RT Splicing".
EL J Biol Chem. 275:2599-2597(2000).
DR EMBL; AF199613; AAF31403.1;
FT NON TER 16
SQ SEQUENCE 16 AA; 1763 MW; 70D5A3075CE769; CD064;
Query Match 28.9% Score 24; DB 4; Length 14;
Best Local Similarity 50.0% Pred. No. 3, Gaps 0;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QV 4 YWYVYSPK 13
DB 7 YWYVYSPK 16
RESULT 10
Q94623 PRELIMINARY; PRT; 15 AA.
AC Q94623
DI 01-FEB-1997 (TrEMBLrel. 02, Created)
DI 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DI 01-NOV-1998 (TrEMBLrel. 04, Last annotation update)
DE MSUSP-2 protein (Fragment).
GN USP.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Lepidoptera;
OC Preytorata; Neoptera; Endopterygota; Lepidoptera; Tortricidae;
OC Spingidae; Spingidae; Spingidae; Manduca.
OX NCBI_TaxID 7130;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EPIDERMIS;
RX MEDLINE=97165493; PubMed=903254;
RA Jindra M.; Huang J.Y.; Malone F.; Asahina M.; Radford J.M.;
RT "Identification and mRNA developmental profiles of two alternative
RT isoforms in the epidermis and wings of Manduca sexta".
RL Insect Mol. Biol. 6:41-53(1997).
DR EMBL; U5902; AAB64235.1;
FT NON TER 8
SQ SEQUENCE 8 AA; 892 MW; F155B5415A75B1; CD564;
Query Match 27.7% Score 23; DB 5; Length 14;
Best Local Similarity 66.7% Pred. No. 6, Gaps 0;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0

QY 11 PKSSG 16

DB 3 PKSSG 8

RESULT 11

Q900X9 PRELIMINARY; PRT; 10 AA.
AC Q900X9 (TREMURel 13, Created)
DT 01-MAY-2000 (TREMURel 13, Last sequence update)
DE Large T antigen (Fragment)
OS Polymavirus JC
OC Viruses, dsRNA viruses, ss RNA stage, Polyomaviridae; Polyomavirus
CX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCN16;
PX MCELINER2097544, PubMed 1061230;
RA Bofill-Mas S., Pina S., Girones R.
RT "Documenting the epidemiologic patterns of polyomaviruses in human populations by studying their presence in urban sewage."
RI Affl. Epidemiol. Microbiol. 135:139-145(2000).
RI EMBL, AF119347; AAF24100.1;
RI NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4056A0771A12163 CRC64;
Query Match 27.71; Score 23; DB 12; Length 10;
Best Local Similarity 55.63; Pred No. 2.9e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0

QY 5 KYZVTPSPX 13

DB 2 KYZVTPSPX 10

RESULT 12

Q900X5 PRELIMINARY; PRT; 10 AA.
AC Q900X5 (TREMURel 13, Created)
DT 01-MAY-2000 (TREMURel 13, Last sequence update)
DE Large T antigen (Fragment)
OS Polymavirus JC
OC Viruses, dsRNA viruses, ss RNA stage, Polyomaviridae; Polyomavirus
CX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCN16;
PX MCELINER2097544, PubMed 1061230;
RA Bofill-Mas S., Pina S., Girones R.
RT "Documenting the epidemiologic patterns of polyomaviruses in human populations by studying their presence in urban sewage."
RI Affl. Epidemiol. Microbiol. 135:139-145(2000).
RI EMBL, AF119347; AAF24100.1;
RI NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4056A0771A12163 CRC64;
Query Match 27.71; Score 23; DB 12; Length 10;
Best Local Similarity 55.63; Pred No. 2.9e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0

QY 5 KYZVTPSPX 13

DB 2 KYZVTPSPX 10

RESULT 13

Q900X3 PRELIMINARY; PRT; 10 AA.

Q900X3 PRELIMINARY; PRT; 10 AA.

AC Q900X3 (TREMURel 13, Created)
DT 01-MAY-2000 (TREMURel 13, Last sequence update)
DE Large T antigen (Fragment)
OS Polymavirus JC
OC Viruses, dsRNA viruses, ss RNA stage, Polyomaviridae; Polyomavirus
CX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCN16;
PX MCELINER2097544, PubMed 1061230;
RA Bofill-Mas S., Pina S., Girones R.
RT "Documenting the epidemiologic patterns of polyomaviruses in human populations by studying their presence in urban sewage."
RI Affl. Epidemiol. Microbiol. 135:139-145(2000).
RI EMBL, AF119347; AAF24100.1;
RI NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4056A0771A12163 CRC64;
Query Match 27.71; Score 23; DB 12; Length 10;
Best Local Similarity 55.63; Pred No. 2.9e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0

QY 5 KYZVTPSPX 13

DB 2 KYZVTPSPX 10

RESULT 14

Q900X1 PRELIMINARY; PRT; 10 AA.
AC Q900X1 (TREMURel 13, Created)
DT 01-MAY-2000 (TREMURel 13, Last sequence update)
DE Large T antigen (Fragment)
OS Polymavirus JC
OC Viruses, dsRNA viruses, ss RNA stage, Polyomaviridae; Polyomavirus
CX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCN16;
PX MCELINER2097544, PubMed 1061230;
RA Bofill-Mas S., Pina S., Girones R.
RT "Documenting the epidemiologic patterns of polyomaviruses in human populations by studying their presence in urban sewage."
RI Affl. Epidemiol. Microbiol. 135:139-145(2000).
RI EMBL, AF119347; AAF24100.1;
RI NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4056A0771A12163 CRC64;
Query Match 27.71; Score 23; DB 12; Length 10;
Best Local Similarity 55.63; Pred No. 2.9e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0

QY 5 KYZVTPSPX 13

DB 2 KYZVTPSPX 10

RESULT 15

Q900W9 PRELIMINARY; PRT; 10 AA.
AC Q900W9 (TREMURel 13, Created)
DT 01-MAY-2000 (TREMURel 13, Last sequence update)
DE Large T antigen (Fragment)
OS Polymavirus JC
OC Viruses, dsRNA viruses, ss RNA stage, Polyomaviridae; Polyomavirus
CX NCBI_TaxID=10632;
Query Match 27.71; Score 23; DB 12; Length 10;
Best Local Similarity 55.63; Pred No. 2.9e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0

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11 40.5 48.8 16 7 AAB60119
12 40 48.2 15 18 AAW23484
13 40 48.2 15 20 AAY34347
14 40 48.2 15 21 AAY57445
15 39 47.0 9 21 AAB26621
16 39 47.0 12 23 ABE74371
17 39 47.0 13 21 AAY58859
18 39 47.0 14 17 AAW24466
19 39 47.0 15 20 AAY43358
20 39 47.0 15 20 AAY29463
21 39 47.0 15 20 AAY18137
22 39 47.0 15 20 AAY18137
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42 39 47.0 15 20 AAY18137
43 39 47.0 15 20 AAY18137
44 39 47.0 15 20 AAY18137
45 39 47.0 15 20 AAY18137

ALIGNMENTS

RESULT 1
AAW45878
15 AAW45878 standard; peptide; 16 AA.
AC AAW45878;
XX 30-GEN-1398 (first entry)
XX Peptide membrane binding element.
XX Membrane binding element, thrombotic disease; inflammatory;
XX complement related disease; soluble peptide.
OS Synthetic.
XX W0802454.A.
XX 22-JAN-1998.
XX 08-JUN-1997; 97WO-EP03715.
XX 15-JUL-1996; 96CP-0014871.
XX (ADPR-) ADPROTECH PLC.
XX Dodd I, Mossakowska DEI, Smith RAG;
XX WPI; 1998-110524/10.
XX Derivatives of soluble poly-peptides bonded to low affinity
XX membrane binding groups providing complement related and
XX thrombotic diseases, providing improved localization at cellular
XX membranes

of results predicted by change to have a
equal to the score of the result being filtered,
plus of the total score distribution.

SUMMARIES

SP	ID	Description
1	AAW45878	Peptide membrane b
2	AAV58955	Membrane binding e
3	ABR1217	Antibacterial memb
4	AAW45881	Peptide membrane b
5	AAV58958	Membrane binding e
6	ABR1240	Antibacterial memb
7	AAW45892	Peptide membrane b
8	ABR1241	Antibacterial memb
9	AAW45893	Peptide membrane b
10	AAV58965	Membrane binding e

XX claim 11; Page 20; 6app; English
XX
XX The present peptide sequence represents a specifically claimed membrane
XX binding element. The invention relates to a solid derivative of a
XX peptide of formula (I), which comprises at least 2 heptapeptides
XX membrane-binding elements (MBE) of low membrane affinity covalently
XX associated with the MBE interact, independently and with thermodynamic
XX addition, with one or more of collagen or artificial membranes exposed
XX to cellular fluid (A). The use of the peptide is particularly suitable with
XX (1) itself, specifically inflammation of any other complement-related
XX disorder (e.g. neurological disease, graft rejection, myocardial
XX infarction, sepsis, rheumatoid arthritis and many others, including
XX application to inducing devices) and thrombolytic disease, but also
XX treat allergy, induce weight loss, to treat ischaemia or asthma and as
XX immuno-modulators for treating multiple sclerosis. (A) are administered
XX orally, intravenously, by injection or inhalation at 0.01-10 (preferably
XX 0.1-10) mg/kg/day
XX
XX Sequence 16 AA.

Query March 100.08; Score 93; DB 19; Length 16;
Best Local Similarity 100.08; Field No. 9.16.06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DGPFFKFFKSPKSSG 16
|||||
DB 1 DGPFFKFFKSPKSSG 16

RESULT 2

AA598955
ID AAYSEARCH standard, Peptide, 16 AA.

AC AAY58855;

DT 08-MAY-2000 (first entry)

XX Membrane binding element used in antiangiogenic therapy.

XX Anti-angiogenic, anti-angiogenesis inhibition, membrane-binding element,
XX Cancer; tumour; therapy.

XX Synthetic.

PN W0200004052-A2.

XX 27-JAN-2000

XX 16-JUL-1999; 94WG-090299

XX 16-JUL-1999; 94GB-0015505.

XX (ADPP-) ADPROTECH PLC.

XX Smith, RAC, Right 3F, Steward M, Cox VF;

XX WF1; 2000-162466/16.

XX New soluble derivative of anti-angiogenic polypeptide useful for
XX treatment of primary or secondary cancer, contains covalently attached
XX membrane-binding elements for targeting.

XX Claim 12; Page 20; 6app; English

XX The present sequence is a claimed example of a lysine-rich peptide
XX membrane binding element (MBE) that can be utilised in novel
XX soluble formulations (1) of anti-angiogenic polypeptides of the
XX invention, for example 2 of more heptapeptides MBEs with low
XX membrane affinity that are covalently attached to a soluble
XX anti-angiogenic polypeptide such as a non-catalytic region of human
XX plasminogen, fragments of related proteins containing kinase
XX domains, fragments of collagen or fibronectin, crystallising

XX antibodies against receptors for angiogenic mediators, and
XX fragments of integrins involved in angiogenesis. The MBEs
XX interact independently with thermodynamic activity, with
XX expression of the vascular endothelium. The provide targeted
XX delivery of the anti-angiogenic peptide to the cell membranes and
XX sites of active angiogenesis, particularly the vascular endothelium,
XX and therefore increase the local concentration and reduce the risk
XX of adverse effects on normal processes elsewhere in the vasculature.
XX They are used in a clinical method of treatment of primary or
XX secondary tumour
XX Sequence 16 AA;
XX Query March 100.08; Score 93; DB 21; Length 16;
XX Best Local Similarity 100.08; Field No. 9.16.06;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DGPFFKFFKSPKSSG 16
|||||
DB 1 DGPFFKFFKSPKSSG 16

RESULT 3

ADPR1237

ID ABB81237 standard; peptide; 16 AA.

XX ABB81237;

XX 20 AUG 2002 (first entry)

XX Antibacterial membrane-binding peptide SFO ID NO:4.

XX Antibacterial; glycopeptide; peptidic membrane associating element;

XX bacterial infection, vancomycin, peptidoglycan biosynthesis inhibition;
XX antibiotic.

XX Synthetic

XX W20020702 A1.

XX 16-MAY-2002.

XX 02-NOV-2001; 2001WO GB04967.

XX 03-NOV-2000; 2000GB 0026924.

XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX (ADPP-) ADPROTECH LTD.

XX Cooper MA, Petley JP;

XX WF1; 2002-471499/50.

XX Antibacterial compound, useful for the treatment of a bacterial

XX infection by e.g. gram positive or negative bacteria, comprises a

XX conjugate of Glycopeptide and peptidic membrane-associating element

XX Claim 7; Page 57; 6app; English.

XX The present invention describes an antibacterial compound (1), comprising
XX a conjugates of glycopeptide and peptidic membrane associating elements,
XX (1) comprises the formula V-L-W-X, where V = a glycopeptide moiety that
XX inhibits peptidoglycan biosynthesis in bacteria; L = a linking group;
XX W = a peptidic membrane-associating element; and X = H or a membrane-

XX infective element. Also described (1) a method of treating or preventing
XX a bacterial infection, comprising the administration of (1), and (2) use
XX of (1) in the manufacture of a medicament for the treatment or prevention
XX of a bacterial infection. (1) are used in the manufacture of a medicament
XX for the treatment of infections. A bacterial infection in a human or
XX animal body, including both the gut lumen and the negative bacteria
XX including Mycobacterium sp., Pseudomonas sp., Bacillus sp., Klebsiella
XX sp., Staphylococcus sp., Vibrio sp., Bacteroides sp., Bacteroides sp.,
XX sp., Neisseria sp., Streptococcus sp., Bacillus sp., and others.

Cy 1 DGPFFRFRFRFRFR 15
|||||
Db 1 DGPFRFRFRFRFR 15

RESULT 6

ABB81240
ID ABB81240 standard; peptide; 16 AA.

AC ABB81240;

XX 20-AUG-2002 (first entry)

XX Antibacterial membrane binding peptide SEQ ID NO.7.

XX Antibacterial, glycopeptide, peptide membrane associating element,

XX Penicillin, infection, vancomycin; peptidoglycan biosynthesis inhibition,

XX antibiotic.

XX Synthetic.

XX W0207246612 A1.

XX 16-MAY-2002.

XX 02 NOV 2001; 2001WG 0694867.

XX 03 NOV 2000; 2000B 0626924.

XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX (ADPR-) ADPRTECH LTD.

XX Cooper MA, Betley JR;

XX WPI, 2002 471499/10.

XX Antibacterial compound, useful for the treatment of a bacterial

XX infection by a glycopeptide or relative bacteria, comprises a

XX mixture of glycopeptide and peptide membrane-associating element.

XX Claim 7; Page 57; 64pp; English.

XX The present invention describes an antibacterial compound (I), comprising

XX a mixture of glycopeptide and peptide membrane-associating element,

XX (I) comprises the formula V LW X, where V is a glycopeptide moiety that

XX inhibits peptidoglycan synthesis in bacteria, and X is a lipid group.

XX W is a peptide membrane associating element, and X is H or a membrane

XX insertion element. Also described is (i) a method of treating or preventing

XX a bacterial infection, comprising the administration of (I), and (ii) use

XX of (I) in the manufacture of a medicament for the treatment or prevention

XX of a bacterial infection. (I) are used in the manufacture of a medicament

XX for the treatment or prophylaxis of a bacterial infection in a human or

XX animal body, including both the gram positive and gram negative bacteria

XX including Mycobacterium sp., Enterobacter sp., Escherichia sp.,

XX Staphylococcus sp., Vibrio sp., Klebsiella sp., Pseudomonas sp.,

XX Pseudomonas sp., Clostridium sp., Pseudomonas sp., Actinomyces sp.,

XX Pseudomonas sp., and Salmonella sp., particularly antibiotic resistant

XX bacterial strains. (I) are also useful as wound treatment agents to

XX prevent adhesion of bacteria to matrix proteins, especially fibrinogen,

XX exposed in wound tissue; and for prophylactic use in dental treatment as

XX an alternative to, or in conjunction with, antibiotic prophylaxis. (I)

XX have a higher binding to bacterial membranes which have a higher

XX proportion of acidic phospholipids than the eukaryotic organisms, also

XX having a higher proportion of membrane associated biosynthesis in bacteria.

XX Vancomycin shows an enhanced antibacterial activity upon derivatisation

XX with (I) and is effective to treat the antibiotic resistant bacterial

XX strains. ABB81240 to ABB81244 represent the antibiotic peptides given in the

XX exemplification of the present invention.

XX Sequence 16 AA;

XX Query Match 92.93; Score 77; EB 23; Length 16;

XX

Best Local Similarity 100.0%; Prod No. 6 to 05;
Matches 10, Conservative 0, Mismatches 0, Indels 0, Gaps 0

Cy 1 DGPFFRFRFRFRFR 15

|||||

Db 1 DGPFRFRFRFRFR 15

RESULT 7

AAW45882

ID AAW45882 standard; peptide; 14 AA.

XX AAW45882;

XX 30-JUN-1998 (first entry)

XX Peptide membrane binding element.

XX Membrane binding element; thrombotic disease; inflammation;

XX Complement-related disease; soluble peptide.

XX Synthetic.

XX WO9802454 A2.

XX 22-JAN-1998.

XX 08-JUL-1997; 97WO-EP03715.

XX 15-JUL-1996; 96GR-0014971.

XX (ADPR-) ADPRTECH PLC.

XX Dadd I, Mossakowska DEL, Smith PAG;

XX WPI, 1999 119524/10.

XX Derivative of soluble poly-peptides, bonded to low affinity

XX membrane binding groups - useful for treating complement-related and

XX thrombotic diseases, providing improved localisation at cellular

XX membranes

XX Claim 11; Page 70; 75pp; English.

XX The present peptide sequence represents a specifically claimed membrane

XX binding element. The invention relates to a soluble derivative (A) of a

XX soluble poly-peptide (B), which contains at least 2 heterologous

XX membrane-binding elements (VSP) of low membrane affinity mutually

XX associated with (i) MRE internal, independently and with thermodynamic

XX activity, with compounds (i) cellular or artificial membrane exposed

XX to extracellular fluids (A) are used to treat disorders treatable with

XX (ii) itself, specifically inflammation or any other complement-related

XX disorder in a neurological disease, graft rejection, myocardial

XX infarction, sepsis, the related antigen and many others, including

XX affluence, swelling diseases, and thrombotic diseases, but also to

XX treat allergy, induce weight loss, or treat ischaemia or asthma and as

XX immuno-moleculars for treating multiple sclerosis. (A) are administered

XX orally, especially, by injection or inhalation at a dose of preferably

XX 0.1 to 100 mg/kg/day.

XX Sequence 14 AA;

XX Query Match 49.03; Score 40.5; NP 19; Length 14;

XX Best Local Similarity 70.0%; Prod No. 14;

XX Matches 10, Conservative 1, Mismatches 1, Indels 1, Gaps 1

Cy 1 DGPFRFRFRFRFR 15

|||||

Db 1 DGPFRFRFRFRFR 15

RESULT 8

ABB81241

RESULT 9
AAW45893
ID AAW45893 standard; peptide; 15 AA.
XX
AC AAW45893;
XX
XX 30-JUN-1998 (first entry)
XX
DE Peptide membrane binding element.
XX
KW Membrane binding element; thrombotic disease; soluble protein
KW Complement-related disease; integral membrane protein; inflammation
XX
OS Synthetic.
XX
PN WO9802454-A2.
XX
PD 22-JAN-1998.
XX
PF 08-JUL-1997; 97WO-EP03715.
XX
PR 15-JUL-1996; 96GB-0014871.
XX
PA (ADPR-) ADPROTECH PLC.
XX
PI Dodd I, Mossakowska DEI, Smith PAB;
XX
XX WPI; 1998-110524/10.
XX
XX Derivation of soluble polypeptides related to low affinity
XX membrane binding groups - useful for treating complement related and
XX thrombotic diseases, providing improved localisation at cellular
XX membranes
XX
PS Claim 21; Page 71; 75pp; English.
XX
XX The present peptide sequence represents a specifically derived membrane
XX binding element. The invention relates to a soluble derivative of a
XX soluble polypeptide (1), which comprises at least 1 heterologous
XX membrane binding elements (MBE) of low membrane affinity, covalently
XX associated with (i) MBE interact, independently and with thermodynamic
XX additivity, with components of cellular or artificial membranes exposed
XX to extracellular fluids. (A) are used to treat disorders treatable with
XX (1) itself, specifically inflammation or any other complement related
XX disorder, e.g. neurological disease, graft rejection, myocardial
XX infarction, sepsis, rheumatoid arthritis and many others, including
XX application to indwelling devices and thrombolytic devices, for a
XX treat allergy, induce weight loss, to treat ischaemia or asthma and as
XX immune modulators for treating multiple sclerosis. (A) are administered
XX orally, topically, by injection or inhalation at 0.001-100 mg/kg/day.
XX
SQ Sequence 15 AA;
XX
XX Query Match 48.8%; Score 40.5; PB 19; Length 15;
XX Best Local Similarity 76.3%; Field No. 19;
XX Matches 10; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
XX
XX 1 DGPFFPPPPPPSPV 13
XX |||||
XX 3 DG-PPPPPPPPV 14
XX
RESULT 10
AAW58865
ID AAW58865 standard; Peptide; 15 AA.
XX
AC AAW58865;
XX
XX 08-MAY-2000 (first entry)
XX
XX Membrane binding element used in anti-angiogenic polypeptides.
XX

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AAW45893
ID AAW45893 standard; peptide; 15 AA.
XX
AC AAW45893;
XX
XX 30-JUN-1998 (first entry)
XX
DE Peptide membrane binding element.
XX
KW Membrane binding element; thrombotic disease; soluble protein
KW Complement-related disease; integral membrane protein; inflammation
XX
OS Synthetic.
XX
PN WO9802454-A2.
XX
PD 22-JAN-1998.
XX
PF 08-JUL-1997; 97WO-EP03715.
XX
PR 15-JUL-1996; 96GB-0014871.
XX
PA (ADPR-) ADPROTECH PLC.
XX
PI Dodd I, Mossakowska DEI, Smith PAB;
XX
XX WPI; 1998-110524/10.
XX
XX Derivation of soluble polypeptides related to low affinity
XX membrane binding groups - useful for treating complement related and
XX thrombotic diseases, providing improved localisation at cellular
XX membranes
XX
PS Claim 21; Page 71; 75pp; English.
XX
XX The present peptide sequence represents a specifically derived membrane
XX binding element. The invention relates to a soluble derivative of a
XX soluble polypeptide (1), which comprises at least 1 heterologous
XX membrane binding elements (MBE) of low membrane affinity, covalently
XX associated with (i) MBE interact, independently and with thermodynamic
XX additivity, with components of cellular or artificial membranes exposed
XX to extracellular fluids. (A) are used to treat disorders treatable with
XX (1) itself, specifically inflammation or any other complement related
XX disorder, e.g. neurological disease, graft rejection, myocardial
XX infarction, sepsis, rheumatoid arthritis and many others, including
XX application to indwelling devices and thrombolytic devices, for a
XX treat allergy, induce weight loss, to treat ischaemia or asthma and as
XX immune modulators for treating multiple sclerosis. (A) are administered
XX orally, topically, by injection or inhalation at 0.001-100 mg/kg/day.
XX
SQ Sequence 15 AA;
XX
XX Query Match 48.8%; Score 40.5; PB 19; Length 15;
XX Best Local Similarity 76.3%; Field No. 19;
XX Matches 10; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
XX
XX 1 DGPFFPPPPPPSPV 13
XX |||||
XX 3 DG-PPPPPPPPV 14
XX
RESULT 10
AAW58865
ID AAW58865 standard; Peptide; 15 AA.
XX
AC AAW58865;
XX
XX 08-MAY-2000 (first entry)
XX
XX Membrane binding element used in anti-angiogenic polypeptides.
XX

CC immunologically reactive with pMCA (peritoneal anti-conceptin);
 CC cytoplasmic antibodies) and detecting formation of a Ag pMCA complex
 CC as indicative of ulcerative colitis. The method is used to diagnose
 CC ulcerative colitis or susceptibility to it. Sequences AAY57341-351
 CC represent pMCA-reactive peptides, derived from human histone H1
 SQ Sequence 15 AA;

Query Match 49 21, 3 19 45, 15 21, Length 171
 Best Local Similarity 58.3%; Pred. No. 187
 Matches 2, Conservative 2, Mismatches 0, Indels 0, Gaps 0.

QY 3 PPKYKYPSPSKS 14
 ||| ||| |||
 DB 3 PPKSAFYTPYKA 14

RESULT 15

AAB26821
 ID AAB26821 standard; peptide; 9 AA.

XX AC AAB26821;

XX DT 23 JAN 2001 (first entry)

XX DE Peptidic membrane binding element.

XX KW Organ perfusion; transplantation; storage; antiinflammatory;

XX KW immunosuppressive; vasotropic; complement activation inhibitor;

XX KW allograft rejection; ischaemia reperfusion injury.

XX OS Synthetic.

XX PN WO200053007-A1.

XX PD 14-SEP-2000.

XX PE 08-MAR-2000; 2000WO GB00834.

XX PR 10-MAR-1999; 99GR-0006503.

XX PA (ADPR-) ADPROTECH LTD.

XX PI Smith RAG, Pratt JP, Sacks SH;

XX DR WPI; 2000-bvl20/57.

XX Preparation for perfusing organ prior to transplantation or storage
 PT comprises soluble binding of a cell the polypeptide which comprises
 PT two heterologous membrane binding elements with low membrane affinity
 PT .

PS Example 2; Page 20; 47pp; English.

XX The present invention relates to formulations and preparations for
 CC perfusing an organ prior to transplantation or storage. The preparation
 CC comprises a soluble derivative of a polypeptide, which has two or more
 CC heterologous membrane binding elements. The membrane binding elements are
 CC capable of interacting, independently and with thermodynamic additivity,
 CC with membrane components of the organ exposed to extracellular perfusion
 CC fluids, and a flush storage solution. The preparation exhibits
 CC antiinflammatory, immunosuppressive and vasotropic activity and works as
 CC a complement activation inhibitor and an inhibitor of cytotoxic T
 CC lymphocyte activity. The preparation is used for preparing an organ prior
 CC to transplantation, storage and for prevention, treatment or
 CC amelioration of a disease or disorder associated with inflammation,
 CC inappropriate complement activation or inappropriate activation of
 CC coagulant or thrombotic processes prior to, during or after
 CC transplantation or storage of an organ. The preparation is useful for
 CC treating hypotactic and acute allograft rejection of transplanted organs
 CC such as kidney, heart, liver or lungs, ischaemia reperfusion injury in
 CC transplanted organs, xenograft rejection and corneal graft rejection. The
 CC present sequence represents a peptidic membrane binding element used in

CC an example of the preparation of the invention.

XX Sequence 9 AA;

Query Match 47 0%, Score 19, DB 21, Length 9;
 Best Local Similarity 77.9%; Pred. No. 7,8e+05;
 Matches 7, Conservative 0, Mismatches 2, Indels 0.

QY 3 PPKYKYPSP 11
 ||| ||| |||
 DB 1 PPKYKYPSP 9

Search completed: March 3, 2003, 06:44:31
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Sequence version 1.1.1
1999 2003 Copyright ©
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1. 146:148 / Seat 4 (1000 seconds)
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1. 146:148 / Seat 4 (1000 seconds)
without alignment
75,411 Million cell updates/sec

20 34 41.0 10 9 US-09-805-301-42
21 34 41.0 10 10 US-09-805-301-43
22 34 41.0 11 9 US-09-805-301-44
23 34 41.0 11 9 US-09-805-301-45
24 34 41.0 12 9 US-09-805-301-46
25 34 41.0 12 9 US-09-805-301-47
26 34 41.0 12 9 US-09-805-301-48
27 34 41.0 13 9 US-09-805-301-49
28 34 41.0 13 9 US-09-805-301-50
29 34 41.0 13 9 US-09-805-301-51
30 34 41.0 13 9 US-09-805-301-52
31 34 41.0 14 9 US-09-805-301-53
32 34 41.0 14 9 US-09-805-301-54
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39 34 41.0 16 9 US-09-805-301-61
40 34 41.0 16 9 US-09-805-301-62
41 33 39.8 12 9 US-09-805-301-63
42 33 39.8 14 9 US-09-805-301-64
43 33 39.8 14 9 US-09-805-301-65
44 33 39.8 16 9 US-09-805-301-66
45 32 38.6 14 9 US-09-805-301-67

ALIGNMENTS

RESULT 1
US-08-910-386A-53
Sequence 53, Application US/08/08/04/04
Patent No. US2002092041A1
GENERAL INFORMATION:
APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Suo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Hulbert, Scott
APPLICANT: Richter, Todd
TITLE OF INVENTION: Procedures and Materials for Controlling
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eight Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-09-805-301-42
FILING DATE: 13-AUG-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/COCKET NUMBER: 023070-5921005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0209
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

```

? MOLECULE TYPE: peptide
? FEATURE:
? NAME/KEY: Modified site
? LOCATION: 13
? OTHER INFORMATION: /product "OTHER"
? OTHER INFORMATION: /note "Xaa = Ile, Met, Thr, Asn, Lys,
? OTHER INFORMATION: Ser or Arg"
? FEATURE:
? NAME/KEY: Modified site
? LOCATION: 14
? OTHER INFORMATION: /product "OTHER"
? OTHER INFORMATION: /note "Xaa = Cys, Ala, Ser or Gly"
US-08 910-386A-53

Query Match 40.4%, Score 43, DB 9, Length 14;
Best Local Similarity 72.0%, Pred. No. 18;
Matches 9, Conservative 2, Mismatches 3, Indels 1, Gaps 0;

QY 3 KKKKKKSPSK 13
DB 2 KKKKKKSPSK 11

RESULT 2
US-09-967-770-16
? Sequence 16, Application US/09967702
? Patent No. US05331457A1
? GENERAL INFORMATION:
? APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
? APPLICANT: TS'EN, Roger
? APPLICANT: GONZALEZ, Jesus
? TITLE OF INVENTION: ISOLATION OF TRANSMEMBRANE PROTEINS BY OPTICAL METHOD
? FILE REFERENCE: PENDING
? CURRENT APPLICATION NUMBER: US/09967702
? PRIOR FILING DATE: 2001-09-28
? PRIOR FILING DATE: 1999-12-13
? PRIOR APPLICATION NUMBER: US 08/063,883
? PRIOR FILING DATE: 1994-01-10
? PRIOR APPLICATION NUMBER: PCT/US96/00652
? PRIOR FILING DATE: 1996-06-05
? FILE REFERENCE: US 08/441,377
? PRIOR FILING DATE: 1995-06-07
? NUMBER OF SEQ ID NOS: 22
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO: 16
? LENGTH: 15
? TYPE: PRT
? ORGANISM: Artificial sequence
? FEATURE:
? OTHER INFORMATION: Isolation modification sequence
US-09 967-772-16

Query Match 47.0%, Score 50, DB 9, Length 15;
Best Local Similarity 80.0%, Pred. No. 18;
Matches 9, Conservative 1, Mismatches 1, Indels 1, Gaps 0;

QY 4 KKKKKKSPSK 13
DB 2 KKKKKKSPSK 11

RESULT 3
US-09-945-249-84
? Sequence 24, Application US/09945249
? Patent No. US05331457A1
? GENERAL INFORMATION:
? APPLICANT: BERLIN, VIVIAN
? APPLICANT: LAVAGNET, VERONIQUE
? APPLICANT: SMITH, SUSAN E.
? TITLE OF INVENTION: ANIMAL AND HUMAN AGENTS FOR IDENTIFYING AND TREATING
? TITLE OF INVENTION: AND USES RELATED THEREOF
? FILE REFERENCE: NIV-074.06

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? CURRENT APPLICATION NUMBER: US/09945249
? CURRENT FILING DATE: 2001-08-31
? PRIOR APPLICATION NUMBER: US 08/441,390
? PRIOR FILING DATE: 2001-01-13
? PRIOR APPLICATION NUMBER: US/771,212
? PRIOR FILING DATE: 1997-12-20
? PRIOR APPLICATION NUMBER: US/631,319
? PRIOR FILING DATE: 1996-04-11
? NUMBER OF SEQ ID NOS: 80
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO: 84
? LENGTH: 15
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Peptide that
? OTHER INFORMATION: is a derivative of the amino acid sequence of the
? OTHER INFORMATION: substrates
US-09-945-249-84

Query Match 47.0%, Score 50, DB 9, Length 15;
Best Local Similarity 80.0%, Pred. No. 18;
Matches 9, Conservative 1, Mismatches 1, Indels 1, Gaps 0;

QY 4 KKKKKKSPSK 13
DB 2 KKKKKKSPSK 11

RESULT 4
US-09-784-818-2
? Sequence 2, Application US/0994818
? Patent No. US05331457A1
? GENERAL INFORMATION:
? APPLICANT: Verck & Co., Inc.
? APPLICANT: Bismarck, Christopher J.
? APPLICANT: Bergman, Jeffrey M.
? TITLE OF INVENTION: PEPTIDE PROTEIN TRANSPORT INHIBITORS
? FILE REFERENCE: US96
? CURRENT APPLICATION NUMBER: US/0994818
? PRIOR FILING DATE: 2001-02-16
? PRIOR APPLICATION NUMBER: US/0994818
? PRIOR FILING DATE: 2000-02-18
? NUMBER OF SEQ ID NOS: 21
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO: 2
? LENGTH: 15
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Completely synthetic sequence
US-09-784-818-2

Query Match 47.0%, Score 50, DB 9, Length 15;
Best Local Similarity 80.0%, Pred. No. 18;
Matches 9, Conservative 1, Mismatches 1, Indels 1, Gaps 0;

QY 4 KKKKKKSPSK 13
DB 2 KKKKKKSPSK 11

RESULT 5
US-09-770-967-2
? Sequence 24, Application US/09967702
? Patent No. US05331457A1
? GENERAL INFORMATION:
? APPLICANT: Merck & Co., Inc.
? APPLICANT: Bismarck, Christopher J.
? APPLICANT: Bergman, Jeffrey M.
? TITLE OF INVENTION: Peptide Protein Transport Inhibitors
? TITLE OF INVENTION: AND USES RELATED THEREOF
? FILE REFERENCE: US96
? CURRENT APPLICATION NUMBER: US/09967702

```



```

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homosapien
US-09-819-522-2

Query Match      47.0% Score 19; DB 10; Length 15;
Best Local Similarity 80.0% Pred. No. 18;
Matches 8; Conservative 1; Mismatches 1; Gaps 0;

QY 4 KKKKKKPSK 13
DE 2 KKKKKKSVK 11

RESULT 8
US-09-757-251-3
; Sequence 3, Application US/0975725;
; Patent No. US2002004217A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: S. Jane deSolms
; APPLICANT: Suzanne C. MacTough
; APPLICANT: Anthony W. Shaw
; TITLE OF INVENTION: INHIBITORS OF PHENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20604Y
; CURRENT APPLICATION NUMBER: US/09/757,251;
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/175,784
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely Synthetic Amino Acid
US-09-757-251-3

Query Match      47.0% Score 39; DB 10; Length 15;
Best Local Similarity 80.0% Pred. No. 18;
Matches 8; Conservative 1; Mismatches 1; Gaps 0;

QY 4 KKKKKKPSK 13
DE 2 KKKKKKSVK 11

RESULT 9
US-09-784-897A-2
; Sequence 2, Application US/09784897A
; Patent No. US20020052363A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Dinsmore, Christopher J.
; APPLICANT: Bergman, Jeffrey M.
; TITLE OF INVENTION: PHENYL-PROTEIN TRANSFERASE INHIBITORS
; FILE REFERENCE: 20497
; CURRENT APPLICATION NUMBER: US/09/784,897A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/183,449
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely Synthetic sequence
US-09-784-897A-2
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homosapien
US-09-819-522-2

Query Match      47.0% Score 19; DB 10; Length 15;
Best Local Similarity 80.0% Pred. No. 18;
Matches 8; Conservative 1; Mismatches 1; Gaps 0;

QY 4 KKKKKKPSK 13
DE 2 KKKKKKSVK 11

RESULT 8
US-09-757-251-3
; Sequence 3, Application US/0975725;
; Patent No. US2002004217A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: S. Jane deSolms
; APPLICANT: Suzanne C. MacTough
; APPLICANT: Anthony W. Shaw
; TITLE OF INVENTION: INHIBITORS OF PHENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20604Y
; CURRENT APPLICATION NUMBER: US/09/757,251;
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/175,784
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely Synthetic Amino Acid
US-09-757-251-3

Query Match      47.0% Score 39; DB 10; Length 15;
Best Local Similarity 80.0% Pred. No. 18;
Matches 8; Conservative 1; Mismatches 1; Gaps 0;

QY 4 KKKKKKPSK 13
DE 2 KKKKKKSVK 11

RESULT 9
US-09-784-897A-2
; Sequence 2, Application US/09784897A
; Patent No. US20020052363A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Dinsmore, Christopher J.
; APPLICANT: Bergman, Jeffrey M.
; TITLE OF INVENTION: PHENYL-PROTEIN TRANSFERASE INHIBITORS
; FILE REFERENCE: 20497
; CURRENT APPLICATION NUMBER: US/09/784,897A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/183,449
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely Synthetic sequence
US-09-784-897A-2
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Query Match 47.0% Score 39; DB 10; Length 15;
Best Local Similarity 80.0%; Pred. No. 18;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKKKKSPSK 13
|||||

DB 2 KKKKKYKTK 11

RESULT 10
US-09-770-981-3
; Sequence 3, Application US/09/770-981
; Patent No. US6000000980A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: S. Jane deSols
; APPLICANT: Gerald E. Stokker
; APPLICANT: Anthony W. Shaw
; TITLE OF INVENTION: INHIBITORS OF PROTEIN PROTEIN TRANSFERASE
; FILE REFERENCE: 20603Y
; CURRENT APPLICATION NUMBER: US/09/770-981
; PRIOR FILING DATE: 2001-01-26
; PRIOR FILING DATE: 2001-01-26
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homosapien
US-09-770-981-3

Query Match 47.0% Score 39; DB 10; Length 15;
Best Local Similarity 80.0%; Pred. No. 18;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKKKKSPSK 13
|||||

DB 2 KKKKKYKTK 11

RESULT 11
US-09-828-325A-3
; Sequence 3, Application US/09/828-325A
; Patent No. US6000000980A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Craig A. Stump
; APPLICANT: Theresa M. Williams
; TITLE OF INVENTION: INHIBITORS OF PROTEIN PROTEIN TRANSFERASE
; FILE REFERENCE: 20603Y
; CURRENT APPLICATION NUMBER: US/09/828-325A
; PRIOR FILING DATE: 2001-09-17
; PRIOR FILING DATE: 2001-09-17
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely Synthetic Amino Acid
US-09-828-325A-3

Query Match 47.0% Score 39; DB 10; Length 15;
Best Local Similarity 80.0%; Pred. No. 18;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKKKKSPSK 13
|||||

DB 2 KKKKKYKTK 11

RESULT 12
US-09-828-325A-3
; Sequence 3, Application US/09/828-325A
; Patent No. US6000000980A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: S. Jane deSols
; APPLICANT: Gerald E. Stokker
; APPLICANT: Anthony W. Shaw
; TITLE OF INVENTION: INHIBITORS OF PROTEIN PROTEIN TRANSFERASE
; FILE REFERENCE: 20603Y
; CURRENT APPLICATION NUMBER: US/09/828-325A
; PRIOR FILING DATE: 2001-09-17
; PRIOR FILING DATE: 2001-09-17
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely Synthetic Amino Acid
US-09-828-325A-3

Query Match 47.0% Score 39; DB 10; Length 15;
Best Local Similarity 80.0%; Pred. No. 18;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKKKKSPSK 13
|||||

DB 2 KKKKKYKTK 11

RESULT 13
US-09-828-325A-3
; Sequence 3, Application US/09/828-325A
; Patent No. US6000000980A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: S. Jane deSols
; APPLICANT: Gerald E. Stokker
; APPLICANT: Anthony W. Shaw
; TITLE OF INVENTION: INHIBITORS OF PROTEIN PROTEIN TRANSFERASE
; FILE REFERENCE: 20603Y
; CURRENT APPLICATION NUMBER: US/09/828-325A
; PRIOR FILING DATE: 2001-09-17
; PRIOR FILING DATE: 2001-09-17
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely Synthetic Amino Acid
US-09-828-325A-3

Query Match 47.0% Score 39; DB 10; Length 15;
Best Local Similarity 80.0%; Pred. No. 18;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKKKKSPSK 13
|||||

DB 2 KKKKKYKTK 11

RESULT 14
US-10-202-189-2
; Sequence 3, Application US/10/202-189
; Publication No. US2003002225A1

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Sequence 1, Appl
Sequence 2, Appl
Sequence 3, Appl
Sequence 4, Appl
Sequence 5, Appl
Sequence 6, Appl
Sequence 7, Appl
Sequence 8, Appl
Sequence 9, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 19, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 25, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 29, Appl
Sequence 30, Appl
Sequence 31, Appl
Sequence 32, Appl
Sequence 33, Appl
Sequence 34, Appl
Sequence 35, Appl
Sequence 36, Appl
Sequence 37, Appl
Sequence 38, Appl
Sequence 39, Appl
Sequence 40, Appl
Sequence 41, Appl
Sequence 42, Appl
Sequence 43, Appl
Sequence 44, Appl
Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-09-041-889-19
Sequence 19, Application US/09041899
Patent No. 6038664
GENERAL INFORMATION:
APPLICANT: Braut, Jonathan
APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Studies Therein, and
TITLE OF INVENTION: Microbial Cellulose Analogs
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4379 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,899
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/837,058
FILING DATE: 11-APR-1997
ATTORNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/CLERK NUMBER: P-PW 3036
TELEPHONE: (619) 535-8949
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-041-889-19

Query Match 48.2% Score 407 DB 3 Length 159
Best Local Similarity 59.3% Freq. No. 57
Matches 7, Conservative 2, Mismatches 1, Indels 1, Gaps 1
US-09-041-889-19
Sequence 1, Appl
Sequence 2, Appl
Sequence 3, Appl
Sequence 4, Appl
Sequence 5, Appl
Sequence 6, Appl
Sequence 7, Appl
Sequence 8, Appl
Sequence 9, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 19, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 25, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 29, Appl
Sequence 30, Appl
Sequence 31, Appl
Sequence 32, Appl
Sequence 33, Appl
Sequence 34, Appl
Sequence 35, Appl
Sequence 36, Appl
Sequence 37, Appl
Sequence 38, Appl
Sequence 39, Appl
Sequence 40, Appl
Sequence 41, Appl

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Db 3 PKRSKATPKKA 14
RESULT 2
US-08-913-058-19
Sequence 19, Application US/08/913-058
Patent No. 6374315
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Targan, Stephan P.
APPLICANT: Eysa, Naik
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Microbial Colitis, and Clinical Outcomes Thereof, Using
TITLE OF INVENTION: Histone H1
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 500
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patent in Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,064
FILING DATE: 27 APR 1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 06/707,638
FILING DATE: 16-FEB-1993
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/622,011
FILING DATE: ABANDONED
CLASSIFICATION: 435
APPLICATION NUMBER: PCT/US/01/02650
FILING DATE: 18-APR-1991
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/615,715
FILING DATE: 20-NOV-1990
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/510,736
FILING DATE: 19-APR-1993 (ABANDONED)
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/AGENT NUMBER: ITSD:412/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 793-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
US 08 429-964-77
Query Match 4367 Score 99 DB 27 Length 10
Best Local Similarity 99.99, Freq. No. 477
Matches 8 Conservative 1; Mismatches 1; Indels 0; Gaps 0
27 4 KKKKKKSK 13
Db 1 KKKKKKSK 10
RESULT 4
US-08-429-964-73
Sequence 73, Application US/08/429-964
Patent No. 6467743
GENERAL INFORMATION:
APPLICANT: BROWN, MICHAEL S.
APPLICANT: GOLSTEIN, JOSEPH L.
APPLICANT: REISS, YUVAL
APPLICANT: JAMES, GUY L.
TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF FARMACOL
TITLE OF INVENTION: TRANSGENIC INHIBITORS
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DUPREE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

```

US-08-985-337A-1
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/032,438
 FILING DATE: 05-DEC-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Muchard, David A.
 REGISTRATION NUMBER: 35,297
 REFERENCE/DOCKET NUMBER: 19833Y
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 908-594-3903
 TELEFAX: 908-594-4720
 TELEX:

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-985-337A-1

Query Match: 47.8%; Score 39; 1B 2; Length 15;
 Best Local Similarity 90.0%; Pred. No. 7;
 Matches 9; Conservative 1; Mismatches 1; Gaps 0;

CY 4 KKKKKKSPK 13
 DB 2 KKKKKKSPK 11

RESULT 6
 US-08-985-124A-1
 Sequence 1, Application US/8995124A
 Patent No. 5972966
 GENERAL INFORMATION:
 APPLICANT: desolms, S. Jane
 TITLE OF INVENTION: INHIBITORS OF FARNESYL-PROTEIN
 TRANSFERASE
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Merck & Co., Inc.
 STREET: P.O. Box 2000, 126 E. Lincoln Ave.
 CITY: Rahway
 STATE: NJ
 COUNTRY: USA
 ZIP: 07065-0900
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/98/095,124A
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/032,438
 FILING DATE: 05-DEC-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Muchard, David A.
 REGISTRATION NUMBER: 35,297
 REFERENCE/DOCKET NUMBER: 19833Y
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 908-594-3903
 TELEFAX: 908-594-4720
 TELEX:

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-985-337A-1
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/032,438
 FILING DATE: 05-DEC-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Muchard, David A.
 REGISTRATION NUMBER: 35,297
 REFERENCE/DOCKET NUMBER: 19833Y
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 908-594-3903
 TELEFAX: 908-594-4720
 TELEX:

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-985-337A-1
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/032,438
 FILING DATE: 05-DEC-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Muchard, David A.
 REGISTRATION NUMBER: 35,297
 REFERENCE/DOCKET NUMBER: 19833Y
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 908-594-3903
 TELEFAX: 908-594-4720
 TELEX:

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-985-337A-1
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/032,438
 FILING DATE: 05-DEC-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Muchard, David A.
 REGISTRATION NUMBER: 35,297
 REFERENCE/DOCKET NUMBER: 19833Y
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 908-594-3903
 TELEFAX: 908-594-4720
 TELEX:

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-985-337A-1
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/032,438
 FILING DATE: 05-DEC-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Muchard, David A.
 REGISTRATION NUMBER: 35,297
 REFERENCE/DOCKET NUMBER: 19833Y
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 908-594-3903
 TELEFAX: 908-594-4720
 TELEX:

US 09-985-320A-1

Query Match: 47.8%, Score 327, EB 2, Length 15,
Best Local Similarity: 80.0%, Field No. 7,
Matches: 8, Conservative: 1, Mismatches: 1, Indels: 0, Gaps: 0

QY 4 PYPYPPYPSK 13
DB 2 PYPYPPYPSK 11

RESULT 7

US 09-985-320A-1

Sequence 1, Application US/66965320A

Patent No. 5977134

GENERAL INFORMATION:

APPLICANT: Ciccarone, Terrence M.

APPLICANT: Halaszko, Wasy

APPLICANT: Halaszko, John H.

APPLICANT: Luma, Jr., William C.

APPLICANT: Stokker, Gerald E.

APPLICANT: Stump, Craig A.

APPLICANT: Williams, Theresa M.

TITLE OF INVENTION: INHIBITORS OF FARNESYL PROTEIN

TITLE OF INVENTION: TRANSFERASE

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.

STREET: P.O. Box 2000, 126 E. Lincoln Ave.

CITY: Rahway

STATE: NJ

COUNTRY: USA

ZIP: 07065-0900

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/98/320A

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/032,579

FILING DATE: 06 DEC 1996

ATTORNEY/AGENT INFORMATION:

NAME: McHard, David A.

REGISTRATION NUMBER: 35,297

REFERENCE/DOCKET NUMBER: 100400

TELECOMMUNICATION INFORMATION:

TELEPHONE: 908 594 3963

TELEFAX: 908-594-4720

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-985-320A-1

Query Match: 47.8%, Score 327, EB 2, Length 15,
Best Local Similarity: 80.0%, Field No. 7,
Matches: 8, Conservative: 1, Mismatches: 1, Indels: 0, Gaps: 0

QY 4 PYPYPPYPSK 13
DB 2 PYPYPPYPSK 11

RESULT 8

US-09-984-732A-1

Sequence 1, Application US/99/04470A

Patent No. 6015817

GENERAL INFORMATION:

APPLICANT: Halaszko, Wasy

APPLICANT: Stump, Craig A.

TITLE OF INVENTION: INHIBITORS OF FARNESYL PROTEIN

TITLE OF INVENTION: TRANSFERASE

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.

STREET: P.O. Box 2000, 126 E. Lincoln Ave.

CITY: Rahway

STATE: NJ

COUNTRY: USA

ZIP: 07065-0900

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/99/044,732A

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/032,106

FILING DATE: 05 DEC 1996

ATTORNEY/AGENT INFORMATION:

NAME: McHard, David A.

REGISTRATION NUMBER: 35,297

REFERENCE/DOCKET NUMBER: 100400

TELECOMMUNICATION INFORMATION:

TELEPHONE: 908-594-3963

TELEFAX: 908-594-4720

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-984-732A-1

Query Match: 47.8%, Score 327, EB 3, Length 15,
Best Local Similarity: 80.0%, Field No. 7,
Matches: 8, Conservative: 1, Mismatches: 1, Indels: 0, Gaps: 0

QY 4 PYPYPPYPSK 13
DB 2 PYPYPPYPSK 11

RESULT 9

US-09-195-578-13

Sequence 13, Application US/09195578

Patent No. 6054466

GENERAL INFORMATION:

APPLICANT: Ciccarone, Terrence M.

APPLICANT: Ciccarone, Terrence M.

APPLICANT: Merck & Co., Inc.

TITLE OF INVENTION: INHIBITORS OF FARNESYL PROTEIN

TITLE OF INVENTION: TRANSFERASE

FILE REFERENCE: 000000

CURRENT APPLICATION NUMBER: US/99/044,732A

CURRENT FILING DATE: 1998-11-18

EARLIER APPLICATION NUMBER: 60/032,106

EARLIER FILING DATE: 1997-12-04

NUMBER OF SEQ ID NOS: 26

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 13

LENGTH: 15

TYPE: PRT

Query 10

Score 39; IP 3; Length 15;
Pred. No. 7;
Matches 8; Mismatches 1; Indels 0; Gaps 0;

Query 11

Score 39; IP 3; Length 15;
Pred. No. 7;
Matches 8; Mismatches 1; Indels 0; Gaps 0;

Query 12

Score 39; IP 3; Length 15;
Pred. No. 7;
Matches 8; Mismatches 1; Indels 0; Gaps 0;

Query 13

Score 39; IP 3; Length 15;
Pred. No. 7;
Matches 8; Mismatches 1; Indels 0; Gaps 0;

Query 14

Score 39; IP 3; Length 15;
Pred. No. 7;
Matches 8; Mismatches 1; Indels 0; Gaps 0;

Query 15

Score 39; IP 3; Length 15;
Pred. No. 7;
Matches 8; Mismatches 1; Indels 0; Gaps 0;

Query 16

Score 39; IP 3; Length 15;
Pred. No. 7;
Matches 8; Mismatches 1; Indels 0; Gaps 0;

Query 17

Score 39; IP 3; Length 15;
Pred. No. 7;
Matches 8; Mismatches 1; Indels 0; Gaps 0;

Query 18

Score 39; IP 3; Length 15;
Pred. No. 7;
Matches 8; Mismatches 1; Indels 0; Gaps 0;

Best Local Similarity 80.0%; Pred. No. 7;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKKKKKSKK 13
DB 2 KKKKKKSKK 11

RESULT 12

US-09-164-482-13
; Sequence 13, Application US/0914442A
; Patent No. 6127390
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: deSols, S. Jane
; APPLICANT: Lumma, William C.
; APPLICANT: Shaw, Anthony W.
; APPLICANT: Sisko, John T.
; APPLICANT: Tucker, Thomas C.
; TITLE OF INVENTION: INHIBITORS OF PHENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20025Y
; CURRENT FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: US/0914442A
; EARLIER FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthesized peptide substrate for
; OTHER INFORMATION: geranylgeranyl protein transferase type 1
US-09-164-482-13

Query Match

Best Local Similarity 47.0%; Score 39; IP 3; Length 15;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKKKKKSKK 13
DB 2 KKKKKKSKK 11

RESULT 13

US-09-332-769-2
; Sequence 2, Application US/09332769
; Patent No. 6172076
; GENERAL INFORMATION:
; APPLICANT: Embrey, Mark W.
; APPLICANT: Perlow, Debra S.
; APPLICANT: Wal, John S.
; APPLICANT: Hofman, Jacob M.
; TITLE OF INVENTION: INHIBITORS OF PHENYL-PROTEIN
; TITLE OF INVENTION: TRANSFERASE
; FILE REFERENCE: 19982Y
; CURRENT FILING DATE: 1999-06-14
; EARLIER APPLICATION NUMBER: US/09332769
; EARLIER FILING DATE: 1998-06-15
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homosapien
US-09-332-769-2

Query Match

Best Local Similarity 47.0%; Score 39; IP 3; Length 15;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKKKKSPSK 13
DB 2 KKKKKSKTK 11

Search completed March 3, 2003, 06:47:20
Job time : 17.667 secs

RESULT 14

US-09-456-153-2
; Sequence 2, Application US/09456153
; Patent No. 6284755
; GENERAL INFORMATION:
; APPLICANT: Desolms, S. Jane
; APPLICANT: Graham, Samuel L.
; APPLICANT: Shaw, Anthony W.
; APPLICANT: Ciccarone, Terrence M.
; APPLICANT: Storker, Gerald E.
; TITLE OF INVENTION: INHIBITORS OF PEPHYL PROTEIN
; TITLE OF INVENTION: TRANSFERASE
; FILE REFERENCE: 20312Y
; CURRENT APPLICATION NUMBER: US/09/456,153
; CURRENT FILING DATE: 1999-12-07
; EARLIER APPLICATION NUMBER: US 60/111,416
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: US 60/129,282
; EARLIER FILING DATE: 1999-04-14
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homosapien
US-09-456-153-2

Query Match 47.0%; Score 39; DB 4; Length 15;
Best Local Similarity 80.0%; Pred. No. 7;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKKKKSPSK 13
DB 2 KKKKKSKTK 11

RESULT 15

US-09-167-180-13
; Sequence 13, Application US/09167180
; Patent No. 6297239
; GENERAL INFORMATION:
; APPLICANT: Desolms, S. Jane
; APPLICANT: Hutchinson, John H.
; APPLICANT: Shaw, Anthony W.
; APPLICANT: Graham, Samuel L.
; APPLICANT: Ciccarone, Terrence M.
; APPLICANT: Merck & Co., Inc.
; TITLE OF INVENTION: INHIBITORS OF PEPHYL PROTEIN TRANSFERASE
; FILE REFERENCE: 19928Y
; CURRENT APPLICATION NUMBER: US/09/167,180
; CURRENT FILING DATE: 1998-10-06
; EARLIER APPLICATION NUMBER: US/602,660
; EARLIER FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homosapien
US-09-167-180-13

Query Match 47.0%; Score 39; DB 4; Length 15;
Best Local Similarity 80.0%; Pred. No. 7;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKKKKSPSK 13
DB 2 KKKKKSKTK 11

ribosomal protein S27a - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C>Date: 29 Aug 1999 #sequence_revision 29 Aug 1999 #text_change 21 Jul 2000

C:Accession: A28144

R:RefSeq: Y.L., Beckstetter, M.

J. Biol. Chem. 263, 4926-4931, 1988

A:Title: Extended reading frame of a ubiquitin gene encodes a stable, conserved, basic p

A:Reference number: A28144, MIM 616043, PMID 343412

A:Accession: A28144

A:Molecule type: Protein

A:Residues: 1-16 (BEE)

C:Comment: This protein is rich in hydrophilic amino acid, and highly heat stable.

C:Keywords: Protein biogenesis

Query Match 28.7% Score 24, DB 2, Length 16;

Best Local Similarity 28.7% Pred. No. 3.7e+01;

Matches 5, Conservative 2, Mismatches 0, Indels 0, Gaps 0.

QY 7 SKKKKK 13

DB 1 AKKKKK 7

RESULT 4

G45681

Ig kappa chain J3 segment has allotype rabbit (fragment)

C:Species: Cytolagus olerarius (javanese rabbit)

C>Date: 29 Aug 1999 #sequence_revision 29 Aug 1999 #text_change 16 Aug 1995

C:Accession: G53275

R:RefSeq: H., Marche, P.A.

Immunogenetics 34, 501-507, 1991

A:Title: Evolution of the rabbit immunoglobulin kappa chain genes.

A:Reference number: A53275, MIM 317166A, PMID 197142

A:Accession: G53275

A:Molecule type: DNA

A:Residues: 1-15 (AFA)

C:Comment: This segment may not be functional because of substitutions in the 7' end

C:Keywords: heterodimer, immunoglobulin

Query Match 21.2% Score 20, DB 2, Length 13;

Best Local Similarity 14.5% Pred. No. 1.1e+01;

Matches 5, Conservative 3, Mismatches 1, Indels 0, Gaps 0.

QY 2 SKKSKKKKK 14

DB 1 STPGSTGK 13

RESULT 5

G45681

orf 61 - phage T6 (fragment)

C:Species: phage T6

C>Date: 29 Aug 1999 #sequence_revision 29 Aug 1999 #text_change 19 Nov-1994

C:Accession: G45681

R:RefSeq: H.F., Stowers, G.D., Pyson, P.B., Alberts, B.M.

J. Virol. 69, 2300-2306, 1995

A:Title: Analysis of five presumptive protein coding sequences clustered between the p

A:Reference number: A45681, MIM 319433, PMID 874347

A:Accession: G45681

A:Molecule type: nucleic acid

A:Residues: 1-16 (SEL)

C:Comment: This segment may not be functional because of substitutions in the 7' end

C:Keywords: heterodimer, immunoglobulin

Query Match 30.1% Score 25, DB 2, Length 16;

Best Local Similarity 28.7% Pred. No. 3.7e+01;

Matches 5, Conservative 0, Mismatches 1, Indels 0, Gaps 0.

QY 8 KKKKKK 13

DB 4 KKKKK 9

RESULT 6

PC4382

Hydrolase 4.1.4.1 (fragment)

N:Alternate names: acid soluble 26K protein

C:Species: Glycine max

C>Date: 29 Aug 1999 #sequence_revision 29 Aug 1999 #text_change 18 Jul 2001

C:Accession: PC4382

R:RefSeq: Y., Harada, K.

Plant Cell Physiol. 39, 1290-1291, 1998

A:Title: Purification and characterization of a 26 kDa protein from

A:Reference number: PC4382, MIM 674400, PMID 9301109

A:Accession: PC4382

A:Molecule type: Protein

A:Residues: 1-14 (KWS)

A:Experimental source: seed

C:Comment: This protein is rich in hydrophilic amino acid, and highly heat stable.

Query Match 28.9% Score 24, DB 2, Length 14;

Best Local Similarity 28.9% Pred. No. 2.7e+01;

Matches 5, Conservative 1, Mismatches 2, Indels 0, Gaps 0.

QY 9 KKKKKKK 15

DB 3 KKKKKKK 10

RESULT 7

I49407

Placental calcium-binding protein, western wall mouse (fragment)

C:Species: Mus musculus (western wild mouse)

C>Date: 29 Aug 1999 #sequence_revision 29 Aug 1999 #text_change 29 Sep 1999

C:Accession: I49407

R:RefSeq: X., Harada, K.

Mamm. Genome 5, 349-355, 1994

A:Title: Purification and characterization of a 40 kDa protein from

A:Reference number: I49407, MIM 343139C, PMID 8043949

A:Accession: I49407

A:Molecule type: DNA

A:Residues: 1-15 (PES)

C:Comment: This segment may not be functional because of substitutions in the 7' end

C:Keywords: calcium binding, EF hand

Query Match 28.9% Score 24, DB 2, Length 15;

Best Local Similarity 28.9% Pred. No. 2.7e+01;

Matches 4, Conservative 2, Mismatches 2, Indels 0, Gaps 0.

QY 6 PSKKKKKK 13

DB 8 PSKKKKKK 15

RESULT 8

S13903

Chaperone, TSP-related - rat

C:Species: Rattus norvegicus (rat)

C>Date: 29 Aug 1999 #sequence_revision 29 Aug 1999 #text_change 1 Nov 1999

C:Accession: S13903

R:RefSeq: F., Gier, P.

Nature 363, 644-649, 1993

A:Title: A TSP-related molecular chaperone from plants refolds pyrolytic

A:Reference number: S13903, MIM 334441, PMID 800715

A:Accession: S13903

A:Molecule type: protein

A:Residues: 1-14 (KWS)

Query Match 27.7% Score 23, DB 2, Length 14;

Best Local Similarity 28.0% Pred. No. 3.7e+01;

Matches 4, Conservative 1, Mismatches 0, Indels 0, Gaps 0.

Query Match 26.5%; Score 22; DB 2; Length 14;
Best Local Similarity 44.4%; Pred. No. 5; Labels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 7 SKKPKK 15
DB 6 AKKPKK 14
RESULT 12
PC7076
Spectrin alpha chain, non-erythroid mouse (fragment)
N:Alternate names: fodrin alpha chain
C:Species: Mus musculus (house mouse)
C:Date: 18-Aug-2000 #sequence_revision 10-Aug-2000 #ext_change 10-Aug-2000
C:Accession: PC7076
R:Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Yamazaki, M.; Maruta, T.; Watanabe, Y.
Electrophoresis 21, 1853-1871, 2000
A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles
A:Reference number: PC7072
A:Accession: PC7076
A:Molecule type: protein
A:Residues: 1-9 <TSU>
A:Experimental source: strain C57BL/6J; Sex: male; Brain, striatum
C:Keywords: brain
Query Match 25.3%; Score 21; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 2; Labels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 5 SPSKKK 11
DB 2 SATPKK 8
RESULT 13
PC0785
NADH dehydrogenase (EC 1.6.99.3) 27K chain - fava bean mitochondrion (fragment)
N:Alternate names: complex I 27K chain, NADH ubiquinone reductase 27K chain
C:Species: mitochondrial Vicia faba (fava bean)
C:Date: 03-May-1994 #sequence_revision 03-Jul-1994 #ext_change 03-Jun-1994
C:Accession: PC0785
R:Letenne, S.; Boutry, M.
Plant Physiol 102, 435-443, 1993
A:Title: Purification and preliminary characterization of the cytochrome complex I NADH
A:Reference number: PC0775; PMID:8415147; PMID:8415148
A:Accession: PC0785
A:Molecule type: protein
A:Residues: 1-10 <LET>
C:Comment: Complex I, mitochondrial NADH ubiquinone reductase, is the first of three
ranging from 54 to 75K.
C:Genetics: This enzyme catalyzes electron transfer from ubiquinol NADH to ubiquinone
C:Keywords: electron transfer; mitochondrial; oxidoreductase
Query Match 25.3%; Score 21; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 5; Labels 0; Gaps 0;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 6 PSKKKK 12
DB 4 PGKKKK 10
RESULT 14
S71300
ICL3 protein - Paramecium tetraurelia (fragment)
C:Species: Paramecium tetraurelia
C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #ext_change 17-Feb-1999
C:Accession: S71300
R:Madoddu, L.; Klotz, G.; Le Caer, J.F.; Boisson, J.
Eur. J. Biochem. 238, 121-129, 1996

Query Match 26.5%; Score 22; DB 2; Length 14;
Best Local Similarity 44.4%; Pred. No. 5; Labels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 7 SKKPKK 15
DB 6 AKKPKK 14
RESULT 12
PC7076
Spectrin alpha chain, non-erythroid mouse (fragment)
N:Alternate names: fodrin alpha chain
C:Species: Mus musculus (house mouse)
C:Date: 18-Aug-2000 #sequence_revision 10-Aug-2000 #ext_change 10-Aug-2000
C:Accession: PC7076
R:Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Yamazaki, M.; Maruta, T.; Watanabe, Y.
Electrophoresis 21, 1853-1871, 2000
A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles
A:Reference number: PC7072
A:Accession: PC7076
A:Molecule type: protein
A:Residues: 1-9 <TSU>
A:Experimental source: strain C57BL/6J; Sex: male; Brain, striatum
C:Keywords: brain
Query Match 25.3%; Score 21; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 2; Labels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 5 SPSKKK 11
DB 2 SATPKK 8
RESULT 13
PC0785
NADH dehydrogenase (EC 1.6.99.3) 27K chain - fava bean mitochondrion (fragment)
N:Alternate names: complex I 27K chain, NADH ubiquinone reductase 27K chain
C:Species: mitochondrial Vicia faba (fava bean)
C:Date: 03-May-1994 #sequence_revision 03-Jul-1994 #ext_change 03-Jun-1994
C:Accession: PC0785
R:Letenne, S.; Boutry, M.
Plant Physiol 102, 435-443, 1993
A:Title: Purification and preliminary characterization of the cytochrome complex I NADH
A:Reference number: PC0775; PMID:8415147; PMID:8415148
A:Accession: PC0785
A:Molecule type: protein
A:Residues: 1-10 <LET>
C:Comment: Complex I, mitochondrial NADH ubiquinone reductase, is the first of three
ranging from 54 to 75K.
C:Genetics: This enzyme catalyzes electron transfer from ubiquinol NADH to ubiquinone
C:Keywords: electron transfer; mitochondrial; oxidoreductase
Query Match 25.3%; Score 21; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 5; Labels 0; Gaps 0;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 6 PSKKKK 12
DB 4 PGKKKK 10
RESULT 14
S71300
ICL3 protein - Paramecium tetraurelia (fragment)
C:Species: Paramecium tetraurelia
C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #ext_change 17-Feb-1999
C:Accession: S71300
R:Madoddu, L.; Klotz, G.; Le Caer, J.F.; Boisson, J.
Eur. J. Biochem. 238, 121-129, 1996

154 (1994).
 IF PMS A COMPLEX WITH HIS THAT BINDS STRONGLY
 PNA (BY SIMILARITY).
 TO THE S19P FAMILY OF PNA-BINDING PROTEINS.

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 (submit.sib.ch).

SW: 404789C9331AA-9.94
 Score 23; DB 1; Length 12;
 Pred. No. 7.444444; Mismatches 0; Gaps 0;
 Mismatches 0; Gaps 0;

Query Match 27.7%; Score 23; DB 1; Length 12;
 Best Local Similarity 56.7%; Pred. No. 9.8e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSSKSP 6
 DQ 3 GSSRDP 8
 |||||
 |||||

Query Match 27.7%; Score 23; DB 1; Length 12;
 Best Local Similarity 56.7%; Pred. No. 9.8e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSSKSP 6
 DQ 3 GSSRDP 8
 |||||
 |||||

Query Match 27.7%; Score 23; DB 1; Length 12;
 Best Local Similarity 56.7%; Pred. No. 9.8e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSSKSP 6
 DQ 3 GSSRDP 8
 |||||
 |||||

Query Match 27.7%; Score 23; DB 1; Length 12;
 Best Local Similarity 56.7%; Pred. No. 9.8e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSSKSP 6
 DQ 3 GSSRDP 8
 |||||
 |||||

Query Match 27.7%; Score 23; DB 1; Length 12;
 Best Local Similarity 56.7%; Pred. No. 9.8e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSSKSP 6
 DQ 3 GSSRDP 8
 |||||
 |||||

Query Match 27.7%; Score 23; DB 1; Length 12;
 Best Local Similarity 56.7%; Pred. No. 9.8e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSSKSP 6
 DQ 3 GSSRDP 8
 |||||
 |||||

Query Match 27.7%; Score 23; DB 1; Length 12;
 Best Local Similarity 56.7%; Pred. No. 9.8e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

154 (1994).
 IF PMS A COMPLEX WITH HIS THAT BINDS STRONGLY
 PNA (BY SIMILARITY).
 TO THE S19P FAMILY OF PNA-BINDING PROTEINS.

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 use agreement. See also: www.ebi.ac.uk/submit/submit.html
 (submit.sib.ch).

SW: 404789C9331AA-9.94
 Score 23; DB 1; Length 12;
 Pred. No. 7.444444; Mismatches 0; Gaps 0;
 Mismatches 0; Gaps 0;

Query Match 27.7%; Score 23; DB 1; Length 12;
 Best Local Similarity 56.7%; Pred. No. 9.8e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSSKSP 6
 DQ 3 GSSRDP 8
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 |||||

Query Match 27.7%; Score 23; DB 1; Length 12;
 Best Local Similarity 56.7%; Pred. No. 9.8e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSSKSP 6
 DQ 3 GSSRDP 8
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 |||||

Query Match 27.7%; Score 23; DB 1; Length 12;
 Best Local Similarity 56.7%; Pred. No. 9.8e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSSKSP 6
 DQ 3 GSSRDP 8
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Query Match 27.7%; Score 23; DB 1; Length 12;
 Best Local Similarity 56.7%; Pred. No. 9.8e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSSKSP 6
 DQ 3 GSSRDP 8
 |||||
 |||||

Query Match 27.7%; Score 23; DB 1; Length 12;
 Best Local Similarity 56.7%; Pred. No. 9.8e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSSKSP 6
 DQ 3 GSSRDP 8
 |||||
 |||||

Query Match 27.7%; Score 23; DB 1; Length 12;
 Best Local Similarity 56.7%; Pred. No. 9.8e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSSKSP 6
 DQ 3 GSSRDP 8
 |||||
 |||||

Query Match 27.7%; Score 23; DB 1; Length 12;
 Best Local Similarity 56.7%; Pred. No. 9.8e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DR EMBL: U39943; AAB41328.1; ...
 DR InterPro: IPR002358; RIBOSOMAL_16_1;
 DR PROSITE: PS00525; RIBOSOMAL_16_1; RAPTAL.
 KW Ribosomal protein; rRNA-binding.
 FT NON-TER 1
 SQ SEQUENCE 16 AA; 1935 MW; ABC1978F5F5R18G0 CR64;

 Query Match
 Best Local Similarity 57.1%; Pred. No. 1, Gap 0;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 QV 7 SKVFFK 13
 DB 10 TREAKK 16
 |||||
 |||||

 RESULT 14
 TRN1 SCHGR STANDARD; PRT; 14 AA.
 AC P82470;
 DT 30-MAY-2000 (Rel. 39, Created;
 DT 30-MAY-2000 (Rel. 39, Last sequence update;
 DT 16-OCT-2001 (Rel. 40, Last annotation update;
 DE Tachykinin-1 (Seq. without tag)
 OS Schistocerca gregaria (Desert locust);
 OC Eukaryota, Metazoa, Arthropoda, Mandibulata, Paleoptera, Hymenoptera;
 OC Insecta; Pterygota, Neoptera; Orthoptera; Orthoptera; Caelifera;
 OC Acridomorpha; Acridoidea; Acrididae; Cystacanthacridinae;
 OC Schistocerca;
 OX NCBI_TaxID-7010;
 RN [1]
 RF SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Midgut;
 RX MEDLINE-2005091; PubMed-1059119;
 RA Veelaert D., Bagderman G., Derua R., Waelkens E., Weenen L.,
 RA Veelaert W., De Loof A., Schoofs L.
 RT "Identification of a new tachykinin from the midgut of the desert
 locust, Schistocerca gregaria, by ESI-Coupled mass spectrometry."
 RL Biochem. Biophys. Res. Commun. 266:230-242 1999.
 CC -!- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPHILIPIC AND PEROXY
 CC -!- OF SPONTANEOUS CONCENTRATIONS AND PHASES OF BINDING TO SURF.
 CC -!- TISSUE SPECIFICITY: MIDGUT.
 CC -!- MASS SPECTROMETRY: MW-143.19; METHOD=Electrospray
 CC -!- SIMILARITY: SIMILAR TO THE COCKROACH LEMTIP 3, A TA KININ
 CC -!- RELATED PEPTIDE ALSO CONFINED TO THE MIDGUT.
 FW Tachykinin, Neuropeptide; Amide.
 FT MOD RES 14 14 AMIDATION.
 SQ SEQUENCE 14 AA; 1436 MW; CA4578C164F02 CR64;

 Query Match
 Best Local Similarity 24.1%; Score 26; DP 1; Length 14;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 QV 10 KKKKPG 15
 DB 4 KKAAPG 9
 |||||
 |||||

 RESULT 15
 UP66 HUMAN STANDARD; PRT; 9 AA.
 AC P30092;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE "Unknown function from the large ribosomal subunit 14; Fragment
 OS Homo sapiens (Human).
 OC Eukaryota, Metazoa, Chordata, Vertebrata, Euteleostomi;
 OC Mammalia, Eutheria, Primates, Catartida; Hominoidea, Homo.
 OX NCBI_TaxID-9606;
 RN [1]
 RF SEQUENCE.
 RC TISSUE=Plasma;

DR EMBL: U39943; AAB41328.1; ...
 DR InterPro: IPR002358; RIBOSOMAL_16_1;
 DR PROSITE: PS00525; RIBOSOMAL_16_1; RAPTAL.
 KW Ribosomal protein; rRNA-binding.
 FT NON-TER 1
 SQ SEQUENCE 16 AA; 1935 MW; ABC1978F5F5R18G0 CR64;

 Query Match
 Best Local Similarity 57.1%; Pred. No. 1, Gap 0;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 QV 7 SKVFFK 13
 DB 10 TREAKK 16
 |||||
 |||||

 RESULT 14
 TRN1 SCHGR STANDARD; PRT; 14 AA.
 AC P82470;
 DT 30-MAY-2000 (Rel. 39, Created;
 DT 30-MAY-2000 (Rel. 39, Last sequence update;
 DT 16-OCT-2001 (Rel. 40, Last annotation update;
 DE Tachykinin-1 (Seq. without tag)
 OS Schistocerca gregaria (Desert locust);
 OC Eukaryota, Metazoa, Arthropoda, Mandibulata, Paleoptera, Hymenoptera;
 OC Insecta; Pterygota, Neoptera; Orthoptera; Orthoptera; Caelifera;
 OC Acridomorpha; Acridoidea; Acrididae; Cystacanthacridinae;
 OC Schistocerca;
 OX NCBI_TaxID-7010;
 RN [1]
 RF SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Midgut;
 RX MEDLINE-2005091; PubMed-1059119;
 RA Veelaert D., Bagderman G., Derua R., Waelkens E., Weenen L.,
 RA Veelaert W., De Loof A., Schoofs L.
 RT "Identification of a new tachykinin from the midgut of the desert
 locust, Schistocerca gregaria, by ESI-Coupled mass spectrometry."
 RL Biochem. Biophys. Res. Commun. 266:230-242 1999.
 CC -!- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPHILIPIC AND PEROXY
 CC -!- OF SPONTANEOUS CONCENTRATIONS AND PHASES OF BINDING TO SURF.
 CC -!- TISSUE SPECIFICITY: MIDGUT.
 CC -!- MASS SPECTROMETRY: MW-143.19; METHOD=Electrospray
 CC -!- SIMILARITY: SIMILAR TO THE COCKROACH LEMTIP 3, A TA KININ
 CC -!- RELATED PEPTIDE ALSO CONFINED TO THE MIDGUT.
 FW Tachykinin, Neuropeptide; Amide.
 FT MOD RES 14 14 AMIDATION.
 SQ SEQUENCE 14 AA; 1436 MW; CA4578C164F02 CR64;

 Query Match
 Best Local Similarity 24.1%; Score 26; DP 1; Length 14;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 QV 10 KKKKPG 15
 DB 4 KKAAPG 9
 |||||
 |||||

 RESULT 15
 UP66 HUMAN STANDARD; PRT; 9 AA.
 AC P30092;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE "Unknown function from the large ribosomal subunit 14; Fragment
 OS Homo sapiens (Human).
 OC Eukaryota, Metazoa, Chordata, Vertebrata, Euteleostomi;
 OC Mammalia, Eutheria, Primates, Catartida; Hominoidea, Homo.
 OX NCBI_TaxID-9606;
 RN [1]
 RF SEQUENCE.
 RC TISSUE=Plasma;

DR EMBL: U39943; AAB41328.1; ...
 DR InterPro: IPR002358; RIBOSOMAL_16_1;
 DR PROSITE: PS00525; RIBOSOMAL_16_1; RAPTAL.
 KW Ribosomal protein; rRNA-binding.
 FT NON-TER 1
 SQ SEQUENCE 16 AA; 1935 MW; ABC1978F5F5R18G0 CR64;

 Query Match
 Best Local Similarity 57.1%; Pred. No. 1, Gap 0;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 QV 7 SKVFFK 13
 DB 10 TREAKK 16
 |||||
 |||||

 RESULT 14
 TRN1 SCHGR STANDARD; PRT; 14 AA.
 AC P82470;
 DT 30-MAY-2000 (Rel. 39, Created;
 DT 30-MAY-2000 (Rel. 39, Last sequence update;
 DT 16-OCT-2001 (Rel. 40, Last annotation update;
 DE Tachykinin-1 (Seq. without tag)
 OS Schistocerca gregaria (Desert locust);
 OC Eukaryota, Metazoa, Arthropoda, Mandibulata, Paleoptera, Hymenoptera;
 OC Insecta; Pterygota, Neoptera; Orthoptera; Orthoptera; Caelifera;
 OC Acridomorpha; Acridoidea; Acrididae; Cystacanthacridinae;
 OC Schistocerca;
 OX NCBI_TaxID-7010;
 RN [1]
 RF SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Midgut;
 RX MEDLINE-2005091; PubMed-1059119;
 RA Veelaert D., Bagderman G., Derua R., Waelkens E., Weenen L.,
 RA Veelaert W., De Loof A., Schoofs L.
 RT "Identification of a new tachykinin from the midgut of the desert
 locust, Schistocerca gregaria, by ESI-Coupled mass spectrometry."
 RL Biochem. Biophys. Res. Commun. 266:230-242 1999.
 CC -!- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPHILIPIC AND PEROXY
 CC -!- OF SPONTANEOUS CONCENTRATIONS AND PHASES OF BINDING TO SURF.
 CC -!- TISSUE SPECIFICITY: MIDGUT.
 CC -!- MASS SPECTROMETRY: MW-143.19; METHOD=Electrospray
 CC -!- SIMILARITY: SIMILAR TO THE COCKROACH LEMTIP 3, A TA KININ
 CC -!- RELATED PEPTIDE ALSO CONFINED TO THE MIDGUT.
 FW Tachykinin, Neuropeptide; Amide.
 FT MOD RES 14 14 AMIDATION.
 SQ SEQUENCE 14 AA; 1436 MW; CA4578C164F02 CR64;

 Query Match
 Best Local Similarity 24.1%; Score 26; DP 1; Length 14;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 QV 10 KKKKPG 15
 DB 4 KKAAPG 9
 |||||
 |||||

 RESULT 15
 UP66 HUMAN STANDARD; PRT; 9 AA.
 AC P30092;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE "Unknown function from the large ribosomal subunit 14; Fragment
 OS Homo sapiens (Human).
 OC Eukaryota, Metazoa, Chordata, Vertebrata, Euteleostomi;
 OC Mammalia, Eutheria, Primates, Catartida; Hominoidea, Homo.
 OX NCBI_TaxID-9606;
 RN [1]
 RF SEQUENCE.
 RC TISSUE=Plasma;

RX MESTINE-0302017; PubMed:1450037;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing";
 RL Electrophoresis 13:707-714(1992).
 CC : MICELLARIEUS: IN THE 2D-GEL THE DETERMINED PT OF THIS UNKNOWN
 CC PROTEIN IS: 5. ITS MW IS: 48 KDa
 DR SWISS 2D PAGE; P30022; HUMAN.
 FT NON-TER 1
 FT NON-TER 9
 SO SEQUENCE 5 AA, 345 MW, 5225PDAAG676447 CDS64;

Query Match 22.98; Score 19; DB 1; Length 9;
 Best Local Similarity 100.0%; Field No. 1.1e+057
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PGD 16
 DB 4 PGD 6

Search completed: March 3, 2003, 06:42:08
 Job time : 7.66667 secs

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1993-2003 Copyright 2003
us-09-214-913-38.closed.rspt
1, 1536128, 2003-03-06 15:06:07
(with new alignments)
152.164 Million cell updates/sec
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23 22 26.5 13 12 Q81797
24 22 26.5 13 12 Q81798
25 22 26.5 13 12 Q81799
26 22 26.5 13 12 Q81800
27 22 26.5 13 12 Q81801
28 22 26.5 13 12 Q81802
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30 22 26.5 13 12 Q81804
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32 22 26.5 13 12 Q81806
33 22 26.5 13 12 Q81807
34 22 26.5 13 12 Q81808
35 22 26.5 13 12 Q81809
36 22 26.5 13 12 Q81810
37 22 26.5 13 12 Q81811
38 22 26.5 13 12 Q81812
39 22 26.5 13 12 Q81813
40 22 26.5 13 12 Q81814
41 22 26.5 13 12 Q81815
42 22 26.5 13 12 Q81816
43 22 26.5 13 12 Q81817
44 22 26.5 13 12 Q81818
45 22 26.5 13 12 Q81819

ALIGNMENTS

RESULT 1
Q9UR86
ID Q9UR86 PRELIMINARY; PRT; 16 AA.
AC Q9UR86;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Class I cytochrome C isoform A (Fragment).
OS Candida parapsilosis (Yeast).
OC Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
OC Saccharomycetales, Microspor Saccharomycetales, Candida.
OX NCBI_TaxID=5480;
RN [1]
RP SEQUENCE.
RY MEDLINE 930559, PubMed=8391313.
RA Cammarand N, Velours J, Denis M, Sverin M,
RT "Isolation, characterization and function of the two type III
RT the yeast Candida parapsilosis.";
RL Biochim. Biophys. Acta 1143:135-141 (1993).
SQ SEQUENCE 16 AA; 1646 MW; 765FF64F75F238E ER04;
Query Match 34.9%; Score 29; JP 31, Length 164
Best Local Similarity 45.5%; Pred. No. 5026-02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1
QY 5 SPSPKPKPKPKPK 15
EI 2 AVYKPKPKPKPK 12
RESULT 2
Q9UR86
ID Q9UR86 PRELIMINARY; PRT; 15 AA.
AC Q9UR86;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 15, Last annotation update)
DE Midline (Fragment).
OS Homo sapiens (Human).

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(with new alignments)
152.164 Million cell updates/sec
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45 22 26.5 13 12 Q81819

SUMMARIES

biochem version 2.1.1
1993-2003 Copyright 2003
us-09-214-913-38.closed.rspt
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(with new alignments)
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42 22 26.5 13 12 Q81816
43 22 26.5 13 12 Q81817
44 22 26.5 13 12 Q81818
45 22 26.5 13 12 Q81819

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CC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostei,
CC Mammalia, Eutheria, Primates, Catarrhini, Hominoidea, Homo
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
FX MEDLINE 9459301, PubMed 941100;
RA Novotny W F, Maffei T, Mehra P L, Milner P G;
RT "Identification of novel hepatitis releasable proteins, as well as the
FT cytochrome c-like and electrophoretic, in human hepatitis plasma";
FT Afr J Lab Med 13:1798-1807 (2003)
SQ SEQUENCE 15 AA, 1527 MW, C34B63787844A2 CPC64;

Query Match 32.5%; Score 27; DB 4; Length 15;
Best Local Similarity 46.2%; Pred No 14e03;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 SESSSESESESESESESE 15
DB 2 AATKRVKGGPS 14

RESULT 3
Q997C1 PRELIMINARY; PRT; 11 AA.
AC Q997C1
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Coat protein (fragment).
OS East African cassava mosaic virus.
OC Viruses, ssRNA viruses, Geminiviridae, Begomovirus.
OX NCBI_TaxID=62079;
RN [1]
RP SEQUENCE FROM N.A.
FX MEDLINE 2163096, PubMed 11172108,
RA Pita J S, Pandey V N, Sengue A, Oti-Nape G W, Ogwal S,
RA Pauget C M;
RT "Recombination, pseudorecombination and synergism of geminiviruses are
RT determinant keys to the epidemic of severe cassava mosaic disease in
RT Uganda.";
SQ SEQUENCE 11 AA, 1516 MW, 17510699AA6374 CPE04;

Query Match 31.3%; Score 26; DB 10; Length 11;
Best Local Similarity 40.0%; Pred No 14e03;
Matches 4; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 12 KPGD 16
DB 3 KPGD 7

RESULT 4
Q997C2 PRELIMINARY; PRT; 13 AA.
AC Q997C2
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 13, Last annotation update)
DE csa peptidase (fragment).
GN SCPA.
OS Streptococcus pyogenes
OC Bacteria, Firmicutes, Bacillus/Clostridium group, Lactobacillales;
OC Streptococcaceae; Streptococcus
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A
RA STRAIN-AP1;
FX MEDLINE 9636075, PubMed 9636075;
RA Berge A, Rasmussen M, Bjorck L;
RT "Identification of an insertion sequence located in a region encoding
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FT vitalence factors of streptococcus pyogenes.";
FT Infect Immun 66:3449-3453 (1998).
RP EMBL: AF064546; AACR768 17; -
DR MEROPS; SC0.020; -
FT NON TER 13
SQ SEQUENCE 13 AA, 1603 MW, 521A97A47E7703 CPE74;

Query Match 31.3%; Score 26; DB 0; Length 13;
Best Local Similarity 46.4%; Pred No 14e03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KKKKKKPGD 16
DB 2 KKKKKKPGD 10

RESULT 5
Q997D0 PRELIMINARY; PRT; 14 AA.
AC Q997D0
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Allinase (EC 4.4.1.4) (fragment)
OS Allium cepa (onion).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliiflorae; Asparagales; Alliaceae;
OC Allium.
OX NCBI_TaxID=4679;
RN [1]
RP SEQUENCE FROM N.A.
FX STEADY EV WASE SHIMAN PPD;
RA Kaminishi A, Nomura K, Ohya T, Kita N;
RT "Cloning of novel fragment of Allinase gene from onion by reverse
RT PCR.";
FT Submitted (JUL2000) to the EMBL/GenBank/DBJ databases.
RP EMBL: AF261193; AAC00509 17; -
KW Inase
FT NON TER 14
SQ SEQUENCE 14 AA, 1573 MW, 235470A38E1B31C0 CPE04;

Query Match 31.3%; Score 26; DB 10; Length 14;
Best Local Similarity 71.4%; Pred No 14e03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSKSPS 7
DB 0 GSKSPS 14

RESULT 6
Q997D5 PRELIMINARY; PRT; 15 AA.
AC Q997D5
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Tumor necrosis factor alpha (fragment).
GN TNFA OR TNF-ALPHA.
OS Homo sapiens (human)
OC Eukaryota, Metazoa; Chordata, Vertebrata, Euteleostei;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=BLVD;
FX Schagdarsurengin U, Glaeser C;
RT "Polymorphism in intron 2 of TNFA, transition A to G.";
FT Submitted (JAN2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
FT TISSUE=BLVD;
RA Schagdarsurengin U, Glaeser C;
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Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 GSKSPSRYFF 12
   | | | | |
Db 3 GHAKFKFKICK 14

RESULT 11
Q56750
ID Q56750 PRELIMINARY; LEN: 14 AA.
AC Q56750;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Pleckstrin protein S19 (Fragment).
OC Western X Phycoplasm.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollitourae;
OC Acheleplasmatales; Acheleplasmataceae; Phycoplasmata.
OX NCBI_TaxID:37764,
   [1]
RN SEQUENCE FROM N.A.
RX MEDLINE 52275243; PubMed:517578;
RA Gudimov D.E., Lee I.M., Pehner S.A., Davis P.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phycoplasmata): a basis for
   their classification."
RL J. Bacteriol. 176:5044-5054(1994).
DF EMBL: D27047; AAA93948.1;
FT NON_TER 1
SQ SEQUENCE 14 AA; 1712 MW; 4004286PAPFFFAAS CRC64;

Query Match 27.7%; Score 23; DB 2; Length 14;
Best Local Similarity 26.7%; Field 1; 4.5e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 GSKSPSRYFF 12
   | | | | |
Db 3 GHAKFKFKICK 14

RESULT 12
Q51574
ID Q51574 PRELIMINARY; PRT: 12 AA.
AC Q51574;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-NOV-1996 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 14 kDa protein (Fragment).
OS Ostertagia ostertagi.
OC Eukaryota; Metazoa; Platyhelminthes; Platyhelminthes; Ostertagiidae.
OX NCBI_TaxID:5117,
   [1]
RN SEQUENCE FROM N.A.
RX MEDLINE 52275243; PubMed:517578;
RA Moore C., Tetley L., Devaney E.;
RT "Identification of abundant worms from the third stage larvae of the
   parasitic nematode, Ostertagia ostertagi."
PL Biochem J 347:761-770(2000)
DR EMBL: AF052049; AAC029.1;
FW Hypothetical protein.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1367 MW; 3679670LCAATVAGY EFO47;

Query Match 26.5%; Score 22; DB 5; Length 12;
Best Local Similarity 26.7%; Field 1; 5.5e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KSPSKN 9
   | | | |
Db 5 QSPSKK 10

RESULT 13

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Q51786
ID Q51786 PRELIMINARY; PRT: 13 AA.
AC Q51786;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA (+sense) strand virus; RNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID:11103;
RN SEQUENCE FROM N.A.
RX MEDLINE 52275243; PubMed:517578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of Hepatitis C virus."
FL EMBL: M84628; AAA45703.1;
FT NON_TER 13
SQ SEQUENCE 13 AA; 1572 MW; 4049011A4QPCGCR CRC64;

Query Match 26.7%; Score 22; DB 12; Length 13;
Best Local Similarity 26.4%; Field 1; 5.5e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 SVSPSPSYFF 13
   | | | | |
Db 2 STNPPQPTK 12

RESULT 14
Q51788
ID Q51788 PRELIMINARY; PRT: 13 AA.
AC Q51788;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA (+sense) strand virus; RNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID:11103;
RN [1]
RX MEDLINE 52275243; PubMed:517578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of Hepatitis C virus."
FL EMBL: M84628; AAA45703.1;
FT NON_TER 13
SQ SEQUENCE 13 AA; 1572 MW; 4049011A4QPCGCR CRC64;

Query Match 26.5%; Score 22; DB 12; Length 13;
Best Local Similarity 26.4%; Field 1; 5.5e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 SVSPSPSYFF 13
   | | | | |
Db 2 STNPPQPTK 12

RESULT 15
Q51783
ID Q51783 PRELIMINARY; PRT: 13 AA.
AC Q51783;

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Seq file version 5.1.1
 1993 2003 compiled 1993
 using sw model
 3, 1046,19 : Search time 46 Seconds
 (with 100 alignments)
 46.144 M, 11.0 cell updates/sec

Seq ID	Seq Name	Seq Length	Seq Type	Seq Description
1	AAW45879	1046	Protein	Peptide membrane b
2	AAW45880	1046	Protein	Membrane binding e
3	AAW45881	1046	Protein	Antibacterial memh
4	AAW45882	1046	Protein	Peptidic membrane
5	AAW45883	1046	Protein	Noctepin-like im
6	AAW45884	1046	Protein	Noctepin-like pe
7	AAW45885	1046	Protein	Peptide which inhi
8	AAW45886	1046	Protein	Peptide which inhi
9	AAW45887	1046	Protein	Fragment of tenase
10	AAW45888	1046	Protein	Fragment of tenase

Summary

1 of results predictability chance to have a
 equal to the score of the result being printed,
 100% of the total score distribution.

Seq ID	Seq Name	Seq Length	Seq Type	Seq Description
11	AAW45879	1046	Protein	Peptide membrane b
12	AAW45880	1046	Protein	Membrane binding e
13	AAW45881	1046	Protein	Antibacterial memh
14	AAW45882	1046	Protein	Peptidic membrane
15	AAW45883	1046	Protein	Noctepin-like im
16	AAW45884	1046	Protein	Noctepin-like pe
17	AAW45885	1046	Protein	Peptide which inhi
18	AAW45886	1046	Protein	Peptide which inhi
19	AAW45887	1046	Protein	Fragment of tenase
20	AAW45888	1046	Protein	Fragment of tenase

ALIGNMENTS

Seq ID	Seq Name	Seq Length	Seq Type	Seq Description
11	AAW45879	1046	Protein	Peptide membrane b
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14	AAW45882	1046	Protein	Peptidic membrane
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16	AAW45884	1046	Protein	Noctepin-like pe
17	AAW45885	1046	Protein	Peptide which inhi
18	AAW45886	1046	Protein	Peptide which inhi
19	AAW45887	1046	Protein	Fragment of tenase
20	AAW45888	1046	Protein	Fragment of tenase

XX
PS Claim 11; Page 20; Title, English
XX
CC The present peptide sequence represents a specifically claimed membrane
CC binding element. The invention relates to a soluble derivative (A) of a
CC soluble polypeptide (P), which comprises at least 2 heterologous
CC membrane-binding elements (MBE) of low membrane affinity covalently
CC associated with (1) MBE interact, independently and with thermodynamic
CC activity, with components of cell-cell or cell-membrane interaction with
CC to extracellular fluids (A) are used to treat disorders treatable with
CC (1) itself, specifically inflammation or any other complement related
CC disorder (e.g. neurological disease, graft rejection, myocardial
CC infection, sepsis, rheumatoid arthritis and many others, including
CC afflictions involving leucocytes and blood clotting diseases, but also
CC treat allergy, induce weight loss, to treat ischaemia or asthma and as
CC immunomodulators for treating multiple sclerosis (A) are administered
CC orally, topically, by injection or inhalation at a 0.1 to preferably
CC 0.1-100 mg/kg/day.
XX
SQ Sequence 15 AA;
Query Match 100.0%, Score 93, DB 19, Length 16;
Best local similarity 100.0%, Pred. No. 12e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DY 1 GSSKSPSSKSKKSKKPPG 16
DB 1 GSSKSPSSKSKKSKKPPG 16
RESULT 2
AAV58856
ID AAV58856 standard; Peptide; 15 AA.
XX
AC AAV58856;
XX
DT 08-MAY-2000 (first entry)
XX
DE Membrane binding element used in anti angiogenic polypeptide.
XX
KW Anti-angiogenic, angiogenesis inhibitor, membrane binding element,
XX cancer; tumour; therapy.
XX
OS Synthetic.
XX
PN W0200004062-A2.
XX
PD 27-JAN-2000.
XX
PF 16 JUN 1999; 99WS 0602252.
XX
PR 16-JUL-1998, 98R 0015505.
XX
PA (ADPR-) ADPRCTECH PLC.
XX
PI Smith RAG, Bright JE, Stewart M, Cox VE,
XX WPI; 2000 165430/16.
XX
PT New soluble derivative of anti angiogenic polypeptide useful for
XX treatment of primary or secondary cancers, contains covalently attached
XX membrane-binding elements for targeting -
XX
PS Claim 12; Page 20; Title, English.
XX
CC The present sequence is a claimed derivative of a lysine-rich peptide
CC membrane binding element (MBE) that can be utilised in novel
CC soluble derivatives (1) of anti-angiogenic polypeptides of the
CC invention. (1) comprise 2 or more heterologous MBEs with low
CC membrane affinity that are covalently attached to a soluble
CC anti-angiogenic polypeptide such as a non catalytic region of human
CC Plasminogen, fragments of related proteins containing kinetic
CC domains, fragments of collagen or fibronectin, heparinising

XX
CC Anionic surface receptors for angiogenic mediators, and
CC antagonists of integrins involved in angiogenesis, the MBEs
CC interact independently with thermodynamic activity, with
CC components of the vascular endothelium. (1) provide targeted
CC delivery of the anti-angiogenic polypeptide to cell membranes and
CC sites of active angiogenesis, particularly the vascular endothelium,
CC and therefore increase the local concentration and reduce the risk
CC of adverse effects on normal processes elsewhere in the vasculature.
XX They are used in a claimed method for treatment of primary or
XX secondary tumour.
XX
SQ Sequence 16 AA;
Query Match 100.0%, Score 93, DB 21, Length 16;
Best local similarity 100.0%, Pred. No. 1.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DY 1 GSSKSPSSKSKKSKKPPG 16
DB 1 GSSKSPSSKSKKSKKPPG 16
RESULT 3
ABB41738
ID ABB41738 standard; peptide; 16 AA.
XX
AC ABB41738;
XX
DT 20-AUG-2002 (first entry)
XX
DE Antibacterial membrane binding peptide SEQ ID NO:5.
XX
KW Antibacterially glycopeptide, glycolytic membrane associated element,
XX bacterial infection, vancomycin, peptidoglycan transpeptidase inhibition,
XX antibiotic.
XX
OS Synthetic.
XX
PN W020000620-A1.
XX
PD 10 MAY 2002.
XX
PF 02 NOV 2001; 2001WO-GB04867.
XX
PR 02 NOV 2000; 2000P 0046924.
XX
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX (ADPR-) ADPRCTECH LTD.
XX
PI Claffer MA, Botley JR;
XX WPI; 2002-471400/50.
XX
PT Antibacterial compound, useful for the treatment of a bacterial
XX infection by oligo gram positive or negative bacteria, comprises a
XX conjugate of glycopeptide and peptide membrane-associated element
XX
PS Claim 1; Page 17; Title, English.
XX
CC The present invention describes an active chemical compound (1) comprising
CC an oligomer of glycopeptide and peptide membrane associated element,
CC (1) comprises the formula V-X, where V is a glycopeptide moiety that
CC inhibits peptidoglycan biosynthesis in bacteria, X is a linking group,
CC W is a peptide membrane-associated element, and X = H or a membrane
CC insertive element. Also described: (i) a method of treating or preventing
CC a bacterial infection, including the administration of (1); and (ii) use
CC of (1) in the manufacture of a medicament for the treatment or prevention
CC of a bacterial infection. (1) are used in the manufacture of a medicament
CC for the treatment or prophylaxis of a bacterial infection, for example
CC against P. ty, including both the gram positive and gram negative bacteria
CC including Mycobacterium. A preferred embodiment of the invention is a
CC conjugate of glycopeptide and peptide membrane-associated element
CC SEQ ID NO:1, consisting of, the following: Aminoacyl

...bacteria spp., particularly antibiotic resistant
...are also useful as xenoantigenic agents to
...to matrix proteins, especially fibronectin,
...and for prophylaxis in dental treatment as
...in combination with antibiotics prophylaxis. (i)
...bacterial membranes which have a higher
...specificity than the existing antibiotics, also
...ion of membrane associated lipoteichoic proteins
...used antimicrobial activity upon derivatisation
...to treat the antibiotic resistant bacterial
...941272 represent peptides derived in the
...invention.

Query Match: 57.8%, Score 48; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 7, 8, 9, 10;
Matches 9; Conservative 0; Mismatches 0; Gaps 0;

14; 1 AA;

QY
DB
1 PSKPKPKPKP 14
1 PSKPKPKPKP 9

...antigen; storage; immunoreactivity;
...; complement; antigenic inhibitor;
...bacteria reperfused.

444.

604.

14; 25 SH;

...than prior to transplantation or storage
...of a soluble protein which comprises
...binding elements with low membrane affinity

1; English.

...to formulations and preparations for
...to transplantation or storage. The preparation
...of a soluble protein which has low mem
...binding elements. The membrane binding elements are
...independently and with thermodynamic affinity;
...of the right of the membrane binding elements
...time solution. The preparation exhibits
...suppressive and vasoconstrictive activity and works as
...inhibitor and an inhibitor of cytotoxic
...preparation as well as regulating an organ prior
...to and for preventing treatment or
...disorder associated with inflammation.

CC inappropriate complement activation or inappropriate activation of
CC coagulant or thrombotic processes prior to, during or after
CC transplantation or storage of an organ; the preparation is useful for
CC treating hyperacute and acute allograft rejection of transplanted organs
CC such as kidney, heart, liver or lungs; ischaemia-reperfusion injury in
CC transplanted organs; xenograft rejection and corneal graft rejection. The
CC present sequence represents a peptide having membrane binding element used in
CC an example of the preparation of the invention.

XX Sequence 9 AA;

Query Match: 57.8%, Score 48; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 7, 8, 9, 10;
Matches 9; Conservative 0; Mismatches 0; Gaps 0;

QY
DB
1 PSKPKPKPKP 14
1 PSKPKPKPKP 9

...antigen; storage; immunoreactivity;
...; complement; antigenic inhibitor;
...bacteria reperfused.

444.

604.

14; 25 SH;

...than prior to transplantation or storage
...of a soluble protein which comprises
...binding elements with low membrane affinity

1; English.

...to formulations and preparations for
...to transplantation or storage. The preparation
...of a soluble protein which has low mem
...binding elements. The membrane binding elements are
...independently and with thermodynamic affinity;
...of the right of the membrane binding elements
...time solution. The preparation exhibits
...suppressive and vasoconstrictive activity and works as
...inhibitor and an inhibitor of cytotoxic
...preparation as well as regulating an organ prior
...to and for preventing treatment or
...disorder associated with inflammation.

14; 25 SH;

...to formulations and preparations for
...to transplantation or storage. The preparation
...of a soluble protein which has low mem
...binding elements. The membrane binding elements are
...independently and with thermodynamic affinity;
...of the right of the membrane binding elements
...time solution. The preparation exhibits
...suppressive and vasoconstrictive activity and works as
...inhibitor and an inhibitor of cytotoxic
...preparation as well as regulating an organ prior
...to and for preventing treatment or
...disorder associated with inflammation.

CC Alternatively, the conjugate has a general formula (C), R1-X-C, R2-C, (C),
 CC where R1, X, R2 and R3 are same as defined in formula A, and salts,
 CC hydrates and their solvates, and C terminally amidated or their
 CC esterified derivatives with suitable organic or inorganic acids.
 CC The conjugate may also be linked to counterions selected from anions,
 CC preferably CH3COO-, CF3COO-, Cl-, SO4^2-, maleate or oleate. Also
 CC included are nucleic acids encoding the peptides, a host cell comprising/
 CC expressing the peptides and antibodies against the peptides.
 CC The peptides and conjugates are useful for the preparation of a
 CC medicament for the treatment and/or prevention of hypotension which is
 CC preferably associated with heart failure, or with intensive diuretic
 CC therapy with thiazide and/or loop diuretics, water diuresis, congestive
 CC heart failure, liver cirrhosis, nephrotic syndrome and hypertension,
 CC multiple organ failure, acute renal failure, disease states associated
 CC with elevated tone of norepinephrine, hypotension, edema associated with
 CC coronary heart failure. The hexapeptides are in part based on the
 CC sequence of formula (P)(V)(W)(PP), a partial agonist of the
 CC 5-HT1A receptor, a G-protein coupled receptor (GPCR) which can be used to
 CC raise antibodies against the conjugates. The present sequence is
 CC an antigenic peptide of the invention.

XX Sequence 10 AA;

Query Match 49.4%; Score 41; DB 21; Length 10;

Best local similarity 100 %, Pos. No. 10;

Matches 9; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

CY 6 PSYVYVYV 13

|||||||

DB 3 PSYVYVYV 10

RESULT 6

ID AAU76079 standard; peptide; 11 AA.

AC AAU76079;

DT 08-MAY-2002 (first entry)

XX Nociceptin-like peptide conjugate 16.

XX Nociceptin, opioid receptor-like 17 (P1), hypotension,
 XX coronary heart failure, diuretic therapy, thiazide, loop diuretic,
 XX water diuresis, congestive heart failure, liver cirrhosis,
 XX nephrotic syndrome, hypertension, multiple organ failure,
 XX acute renal failure, hypokalaemia, oedema.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "Cys is hydroxylated"

FT Modified-site 11 /note= "Lys is amidated"

XX W0000100104 A1.

XX 27 DEC 2001.

XX 15-JUN 2001; 2001W0 US10113

XX 16-JUN 2000; 2000PK 0000944.

XX 05-OCT-2000; 2000US-0001485.

XX 06-DEC-2000; 2000US 001471P.

XX 13-JUN 2001; 2001W0-US41004.

XX (ZEAL) ZEALAND PHARM AC.

XX Larsen BD, Petersen JS, Kapusta DP, Harlow PW;

XX WPI; 2000 171551/200.

XX

PT New peptide conjugate useful for preparing medicament for treating
 PT congestive heart failure, liver cirrhosis, nephrotic syndrome and
 PT hypertension comprises modified R and/or C terminals

XX Example 1, Page 46, copy, English.

XX The invention relates to a peptide conjugate of the general formula (A),
 CC R1-X-C, R2-C, (A), where X is a hexapeptide of formula (B);
 CC R1-A2-A3-A4-A5-A6-R3; A1-R1, R2-R2, or H; A2-R2, W, or F; A3-R3, Y,
 CC X, W or F; A4-R4, R5-R5, A5-R5, A6-R6, V, W, L, V, L, and A6-R6, F, R or
 CC H. Each amino acid residue in the hexapeptide may be in the L or D
 CC form, Z and Z' is a charged residue, chain of 4-20 amino acid residues
 CC having the E or L configuration or is missing provided that not both of Z
 CC and Z' are missing, R1, R2, R3, R4, R5, R6, R7, R8, R9, R10, R11, R12, R13,
 CC R14, R15, R16, R17, R18, R19, R20, R21, R22, R23, R24, R25, R26, R27, R28,
 CC where the conjugate being of a linearly linked amino acid residue, it
 CC is a salt, hydrate and their solvates, and C-terminally amidated
 CC or their esterified derivatives with suitable organic or inorganic acids.
 CC Alternatively, the conjugate has a general formula (C), R1-X-Z-R2 (C),
 CC where R1, X, Z and R2 are same as defined in formula A, and salts,
 CC hydrates and their solvates, and C-terminally amidated or their
 CC esterified derivatives with suitable organic or inorganic acids.
 CC The conjugate may also be linked to counterions selected from anions,
 CC preferably CH3COO-, CF3COO-, Cl-, SO4^2-, maleate or oleate. Also
 CC included are nucleic acids encoding the peptides, a host cell comprising/
 CC expressing the peptides and antibodies against the peptides.
 CC The peptides and conjugates are useful for the preparation of a
 CC medicament for the treatment and/or prevention of hypotension which is
 CC preferably associated with heart failure, or with intensive diuretic
 CC therapy with thiazide and/or loop diuretics, water diuresis, congestive
 CC heart failure, liver cirrhosis, nephrotic syndrome and hypertension,
 CC multiple organ failure, acute renal failure, disease states associated
 CC with elevated tone of norepinephrine, hypotension, edema associated with
 CC coronary heart failure. The hexapeptides are in part based on the
 CC sequence of formula (P)(V)(W)(PP), a partial agonist of the
 CC 5-HT1A receptor, a G-protein coupled receptor (GPCR) which can be used to raise
 CC antibodies against the conjugates. The present sequence is
 CC a peptide conjugate of the invention.

XX Sequence 11 AA;

Query Match 49.4%; Score 41; DB 23; Length 11;

Best local similarity 100 %, Pos. No. 11;

Matches 9; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

CY 6 PSYVYVYV 13

|||||||

DB 4 PSYVYVYV 11

RESULT 7

AAU71160

ID AAU71160 standard; protein; 12 AA.

XX AAU71160;

XX 04 OCT 2000 (updated)

XX 04-APR-1991 (first entry)

XX Peptide which inhibits the binding of fibrinogen to platelets.

XX Fibrinogen; platelets; cancer; cell attachment;

XX Synthetic.

XX SF0000957-A.

XX 06 MAY 1987.

XX 27 OCT 1946; 00EP-0009335.

XX 26-OCT-1946, 00RS 0701072.

XX

CC phenomena such as cancer.
CC (Updated on 03-OCT-2002 to add missing GS field.)
XX
SQ Sequence 12 AA;

Query Match 48.2%; Score 40; DP 8; Length 12;
Best Local Similarity 88.9%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 XXXXXPGD 16
DB 3 XXXXXRGC 11
|||||
RESULT 9
AAR24217
ID AAR24217 standard; Protein; 12 AA.
XX
AC AAR24217;
XX
DT 18 NOV-1992 (first entry)
XX
DE Fragment of tenascin-related peptide.
XX
KW Tenascin, related peptide, cell attachment, antibody, anti, protein;
KW tumour metastasis; solid matrix; prosthetic device; vascular graft;
KW percutaneous device.
XX
FN WO9207872-A.
XX
PD 14-MAY-1992.
XX
PF 29-OCT-1991; 91PC-0508218.
XX
PR 30-OCT-1990; 90IS-0605667.
PR 29-OCT-1990; 90IS-0605920.
XX
PA (CALB-) CALIFORNIA INST BIOLOGICAL RES.
XX
PI Bourdon MA;
XX
WT; 1992 12345678.
XX
PT New tenascin-related peptides - modulate cell attachment;
PT tenascin, useful in inhibition of tumour metastasis and
PT angiogenesis
XX
PS Disclosure; page 6; 60pp; English.
XX
CC The peptide may form an N- or C terminal fragment of the tenascin
CC peptide of AAR24192, which is a tenascin related peptide. This
CC peptide mimics the ability of tenascin to promote cell attachment.
CC The peptide and antibodies raised to it can be used to modulate cell
CC attachment to tenascin, esp. to inhibit tumour metastasis and
CC angiogenesis. The peptide is pref. attached to a solid matrix, eg
CC collagen, fibrin, cellulose, polyester, glass, synthetic resin, long chain
CC polymers, etc. The peptide is pref. attached to a solid matrix, eg
CC to a solid matrix forming a prosthetic device, percutaneous device,
CC vascular graft, etc. For topical admin. it is formulated into a
CC lotion, saline, gel, colloid, powder etc.
XX
SQ Sequence 12 AA;

Query Match 48.2%; Score 40; DP 8; Length 12;
Best Local Similarity 88.9%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 XXXXXPGD 16
DB 3 XXXXXRGC 11
|||||
RESULT 10

CC phenomena such as cancer.
CC (Updated on 03-OCT-2002 to add missing GS field.)
XX
SQ Sequence 12 AA;

Query Match 48.2%; Score 40; DP 8; Length 12;
Best Local Similarity 88.9%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 XXXXXPGD 16
DB 3 XXXXXRGC 11
|||||
RESULT 9
AAR24217
ID AAR24217 standard; Protein; 12 AA.
XX
AC AAR24217;
XX
DT 18 NOV-1992 (first entry)
XX
DE Fragment of tenascin-related peptide.
XX
KW Tenascin, related peptide, cell attachment, antibody, anti, protein;
KW tumour metastasis; solid matrix; prosthetic device; vascular graft;
KW percutaneous device.
XX
FN WO9207872-A.
XX
PD 14-MAY-1992.
XX
PF 29-OCT-1991; 91PC-0508218.
XX
PR 30-OCT-1990; 90IS-0605667.
PR 29-OCT-1990; 90IS-0605920.
XX
PA (CALB-) CALIFORNIA INST BIOLOGICAL RES.
XX
PI Bourdon MA;
XX
WT; 1992 12345678.
XX
PT New tenascin-related peptides - modulate cell attachment;
PT tenascin, useful in inhibition of tumour metastasis and
PT angiogenesis
XX
PS Disclosure; page 6; 60pp; English.
XX
CC The peptide may form an N- or C terminal fragment of the tenascin
CC peptide of AAR24192, which is a tenascin related peptide. This
CC peptide mimics the ability of tenascin to promote cell attachment.
CC The peptide and antibodies raised to it can be used to modulate cell
CC attachment to tenascin, esp. to inhibit tumour metastasis and
CC angiogenesis. The peptide is pref. attached to a solid matrix, eg
CC collagen, fibrin, cellulose, polyester, glass, synthetic resin, long chain
CC polymers, etc. The peptide is pref. attached to a solid matrix, eg
CC to a solid matrix forming a prosthetic device, percutaneous device,
CC vascular graft, etc. For topical admin. it is formulated into a
CC lotion, saline, gel, colloid, powder etc.
XX
SQ Sequence 12 AA;

Query Match 48.2%; Score 40; DP 8; Length 12;
Best Local Similarity 88.9%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 XXXXXPGD 16
DB 3 XXXXXRGC 11
|||||
RESULT 10

```

AAE24220
ID  AAR44220 standard; Protein, 12 AA.
XX
AC  AAR24220;
XX
DT  18-NOV 1992 (first entry)
XX
DE  Fragment of tenascin related peptide.
XX
KW  Tenascin, related peptide, cell attachment, antibody, angiogenesis,
KW  tumour metastasis, solid matrix, prosthetic device, vascular graft,
KW  percutaneous device.
XX
PN  WO9207872-A.
XX
XX  14-MAY-1992.
XX
XX  29-OCT-1991; 91WO-US08018.
XX
XX  30-OCT-1990; 90US-065667.
XX  29-OCT-1990; 90US-0605920.
XX
PA  (CALIF) CALIFORNIA INST RESEARCH, RES
XX
XX  Boulder CO,
XX
XX  WPI, 1992 1990-1991.
XX
PT  New tenascin related peptides modulate cell attachment to
PT  tenascin, useful in inhibition of tumour metastasis and
PT  angiogenesis
XX
PS  Disclosure; page 8; 60pp; English.
XX
XX  The peptide may form with its C-terminal fragment of the protein
XX  peptide of AAR44220, which is a tenascin-related peptide. This
XX  peptide mimics the ability of tenascin to promote cell attachment
XX  to the peptide and antibodies raised to it can be used to modulate cell
XX  attachment to tenascin, esp. to inhibit tumour metastasis and
XX  angiogenesis. The peptide is preferably attached to a solid matrix, eg
XX  collagen, nitrocellulose, polystyrene, glass, synthetic resin, long chain
XX  polyacrylate or synthetic resin fibre. It is especially operatively linked
XX  to a solid matrix forming a prosthetic device, percutaneous device,
XX  vascular graft, etc. For topical admin. it is formulated for oral
XX  solution, saline, gel, colloid, powder etc
XX
SQ  Sequence 12 AA;
    Query Match 45.2%; Score 40; DB 1; Length 12;
    Best Local Similarity 98.9%; Pred. NO. 17;
    Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
    QY  9 KKKKKKKKK 16
    DB  3 KKKKKKKKK 11
    RESULT 11
    AAY90160
    ID  AAY90160 standard; peptide; 11 AA.
    XX
    AC  AAY90160;
    XX
    DT  21-SEP-2000 (first entry)
    XX
    DE  UPAR targeting sequence with spacers #10.
    XX
    KW  ligand epitope, UPAR, alkaline type plasminogen activator receptor,
    KW  adenovirus, hexon, hexon loop, hexon loop, peripheral artery disease,
    KW  recombinant adenovirus vector, tumour, restenosis, gene therapy, asthma,
    KW  epithelial cell proliferation inhibitor, primary artery disease,
    KW  obesity, neurodegenerative diseases, infection, autoimmune disease, HIV,
    KW  cell death, hepatitis, liver modified virus
    XX
    XX  Adenovirus sp.
    XX  WO2000012748-A1.
    XX
    PD  09-MAR-2000.
    XX
    PF  27 AUG 1999; 99WO 1901524.
    XX
    XX  2 AUG 1999; 99WO 1901524.
    PA  (AVET ) AVENTIS PHARMA SA.
    XX
    PI  Vigne B, Dedieu J, Latta M, Yeh P, Porticaudet M;
    XX  WPI; 2000 054441/22.
    XX
    PT  Urokinase type plasminogen activator receptor (UPAR) targeted
    PT  adenovirus vectors having modified hexon loop and H1 loops and modified
    PT  fiber proteins useful for targeted gene therapy to treat cancer or
    PT  restenosis
    XX
    PS  Claim 15, Page 69, 128pp; English.
    XX
    XX  This sequence represents a targeting sequence for UPAR, and is flanked
    XX  by linker. The invention relates to an adenovirus from which a
    XX  linker of the hexon loop or H1 loop is replaced with a binding
    XX  peptide, or targeting sequence, flanked by connecting amino acid spacers,
    XX  to functionally display its binding specificity at the capsid surface.
    XX  The invention also relates to a recombinant adenovirus vector where a
    XX  binding peptide, or targeting sequence, is connected to the C-terminus of
    XX  the fiber by a connecting spacer, or linker, so as to functionally
    XX  display its binding specificity at the capsid surface. The adenovirus or
    XX  recombinant adenovirus vector can be used to preferentially express a
    XX  gene in a target cell, especially a cell that expresses a UPAR. The
    XX  targeted adenovirus vector preferably carries a heterologous gene
    XX  encoding a gene for treatment of a tumour or restenosis. The targeted
    XX  adenovirus vector is useful for gene therapy treatment of a disease, and
    XX  for manufacturing a medicine used in gene therapy treatment of a disease.
    XX  The virus can be used to inhibit smooth muscle cell proliferation,
    XX  to treat proliferative diseases, to treat arteriosclerosis, atherosclerosis,
    XX  neurodegenerative diseases, infectious diseases, autoimmune diseases, asthma, HIV,
    XX  hepatitis, and diabetes. The viruses are particularly targeted against a
    XX  urokinase type plasminogen activator receptor (UPAR). The adenoviruses
    XX  are typically modified without adversely impacting productivity of the
    XX  vectors.
    XX
    SQ  Sequence 11 AA;
    Query Match 45.0%; Score 39, DB 21, Length 11;
    Best Local Similarity 89.0%; Pred. NO. 21;
    Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
    QY  7 SKKKKKKK 15
    DB  2 SKKKKKKK 10
    RESULT 12
    AAY90169
    ID  AAY90169 standard; peptide, 13 AA.
    XX
    AC  AAY90169;
    XX
    DT  21-SEP-2000 (first entry)
    XX
    DE  UPAR targeting sequence with spacers #19.
    XX
    KW  ligand epitope, UPAR, alkaline type plasminogen activator receptor,
    KW  adenovirus, hexon, hexon loop, hexon loop, peripheral artery disease,
    KW  recombinant adenovirus vector, tumour, restenosis, gene therapy, asthma,
    KW  epithelial cell proliferation inhibitor, primary artery disease,
    KW  obesity, neurodegenerative diseases, infection, autoimmune disease, HIV,
    KW  cell death, hepatitis, liver modified virus

```


XX This sequence is a heparin sulphate proteoglycan (HSPG) targeted
XX invention referred to as adenovirus vector which at
XX least a part of the heparin HSPG or HSPG is replaced with a binding
XX peptide, or targeting sequence, flanked by connecting amino acid spacers,
XX so functionally display its binding specificity at the desired surface.
XX The invention also relates to a heparin HSPG which is modified where a
XX binding peptide, or targeting sequence, is connected to the C-terminus of
XX the fiber by a connecting spacer, or linker, so as to functionally
XX recombine adenovirus vector for targeting, preferably, to, replacing a
XX gene in a target cell, especially a cell that expresses a HSPG, the
XX targeted adenovirus vector preferably comprises a heterologous gene
XX encoding a gene for treatment of a tumor or restenosis. The targeted
XX adenovirus vector is useful for gene therapy treatment of a disease, and
XX for manufacturing a medicine used in gene therapy treatment of a disease.
XX The viruses can also be used to inhibit smooth muscle cell proliferation,
XX to treat peripheral artery diseases, coronary artery disease, obesity,
XX neurodegenerative diseases, infections, autoimmune diseases, asthma, HIV,
XX thrombosis, and diabetes. The viruses are particularly targeted against a
XX proteinase type I or II, or a cell that expresses a proteinase type I or II,
XX are tropism-modified without adversely impacting productivity of the
XX vectors.

XX SQ Sequence 13 AA;
XX
XX Query Match 47.0%; Score 19; DB 21; Ident 0; Gaps 0;
XX Best Local Similarity 88.9%; Pred. No. 26;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0

XX QY 7 SKKKKKKPG 15
XX |||||
XX 3 SKKKKKKPG 11

XX RESULT 14
XX AAW45878
XX 1D AAW45878 standard; Peptide; 16 AA.
XX AC AAW45878;
XX XX
XX 30-JUN-1998 (first entry)
XX DE Peptide membrane binding element.
XX XX
XX Membrane binding element, therapeutic disease, inflammation
XX KW complement related disease; soluble peptide.
XX XX

XX This sequence is a heparin sulphate proteoglycan (HSPG) targeted
XX invention referred to as adenovirus vector which at
XX least a part of the heparin HSPG or HSPG is replaced with a binding
XX peptide, or targeting sequence, flanked by connecting amino acid spacers,
XX so functionally display its binding specificity at the desired surface.
XX The invention also relates to a heparin HSPG which is modified where a
XX binding peptide, or targeting sequence, is connected to the C-terminus of
XX the fiber by a connecting spacer, or linker, so as to functionally
XX recombine adenovirus vector for targeting, preferably, to, replacing a
XX gene in a target cell, especially a cell that expresses a HSPG, the
XX targeted adenovirus vector preferably comprises a heterologous gene
XX encoding a gene for treatment of a tumor or restenosis. The targeted
XX adenovirus vector is useful for gene therapy treatment of a disease, and
XX for manufacturing a medicine used in gene therapy treatment of a disease.
XX The viruses can also be used to inhibit smooth muscle cell proliferation,
XX to treat peripheral artery diseases, coronary artery disease, obesity,
XX neurodegenerative diseases, infections, autoimmune diseases, asthma, HIV,
XX thrombosis, and diabetes. The viruses are particularly targeted against a
XX proteinase type I or II, or a cell that expresses a proteinase type I or II,
XX are tropism-modified without adversely impacting productivity of the
XX vectors.

XX SQ Sequence 13 AA;
XX
XX Query Match 47.0%; Score 19; DB 21; Ident 0; Gaps 0;
XX Best Local Similarity 88.9%; Pred. No. 26;
XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0

XX QY 7 SKKKKKKPG 15
XX |||||
XX 3 SKKKKKKPG 11

XX RESULT 14
XX AAW45878
XX 1D AAW45878 standard; Peptide; 16 AA.
XX AC AAW45878;
XX XX
XX 30-JUN-1998 (first entry)
XX DE Peptide membrane binding element.
XX XX
XX Membrane binding element, therapeutic disease, inflammation
XX KW complement related disease; soluble peptide.
XX XX

```

OS Synthetic.
XX WO9802454-A2.
XX 27-JAN-1998
XX 08-JUL-1997; 97WO-BP03715.
XX 15-JUL-1998; 98GB-0014971.
XX (ADPP-) APPOTTECH PLC.
XX Dodd I, Mossakowska DEI, Smith RAG;
XX WPI, 1998-110534/10.
XX Derivatives of soluble polypeptide(s) related to low affinity
PT membrane binding groups - useful for treating complement-related and
PT thrombotic diseases, providing improved localisation at cellular
PT membranes
XX Claim 11, Page 70, 75pp, English.
XX The present peptide sequence represents a specifically claimed membrane
XX binding element. The invention relates to a soluble derivative (A) of a
XX soluble polypeptide (B), which comprises at least 2 heterologous
XX membrane binding elements (MBE) of low membrane affinity covalently
XX associated with (i) MBE interact, independently and with thermodynamic
XX additivity, with components of cellular or artificial membranes exposed
XX to extracellular fluids. (A) are used to treat disorders treatable with
XX (i) itself, specifically inflammation or any other complement-related
XX disorder (e.g. rheumatoid disease, graft rejection, myocardial
XX infarction, sepsis, thrombotic arthritis and many others), including
XX application to inducing weight loss, to treat ischaemia or asthma and as
XX immunomodulators for treating multiple sclerosis. (A) are administered
XX orally, topically, by injection or inhalation at 0.01-10 (preferably
XX 0.1-10) mg/kg/day.
XX Sequence 16 AA;
XX Query Match. 47.0%, Score 30, PP 10, Length 16;
XX Best Local Similarity 77.8%; Pred. No. 32;
XX Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 PSKKKKKKP 14
DB | |||||
DB 3 PKKKKKKSP 11
RESULT 15
AAW45881
XX ID AAW45881 standard; peptide; 16 AA.
XX AC AAW45881;
XX 30-JUN-1998 (first entry)
XX Peptide membrane binding element.
XX Membrane binding element; thrombotic disease; inflammation;
XX complement-related disease; soluble peptide.
XX Synthetic.
XX WO9802454-A2.
XX 27-JAN-1998.
XX 08-JUL-1997; 97WO-BP03715.
XX 15-JUL-1998; 98GB-0014971
XX
XX
XX
XX
XX
XX

```

```

PA (ADPP-) APPOTTECH PLC
XX Dodd I, Mossakowska DEI, Smith RAG;
XX WPI, 1998-110534/10.
XX Derivatives of soluble polypeptide(s) related to low affinity
PT membrane binding groups - useful for treating complement-related and
PT thrombotic diseases, providing improved localisation at cellular
PT membranes
XX Claim 11, Page 70, 75pp, English.
XX The present peptide sequence represents a specifically claimed membrane
XX binding element. The invention relates to a soluble derivative (A) of a
XX soluble polypeptide (B), which comprises at least 2 heterologous
XX membrane binding elements (MBE) of low membrane affinity covalently
XX associated with (i) MBE interact, independently and with thermodynamic
XX additivity, with components of cellular or artificial membranes exposed
XX to extracellular fluids. (A) are used to treat disorders treatable with
XX (i) itself, specifically inflammation or any other complement-related
XX disorder (e.g. rheumatoid disease, graft rejection, myocardial
XX infarction, sepsis, thrombotic arthritis and many others), including
XX application to inducing weight loss, to treat ischaemia or asthma and as
XX immunomodulators for treating multiple sclerosis. (A) are administered
XX orally, topically, by injection or inhalation at 0.01-10 (preferably
XX 0.1-10) mg/kg/day.
XX Sequence 16 AA;
XX Query Match. 47.0%, Score 30, PP 10, Length 16;
XX Best Local Similarity 77.8%; Pred. No. 32;
XX Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 PSKKKKKKP 14
DB | |||||
DB 3 PKKKKKKSP 11
Search completed: March 3, 2003, 06:44:32
Ref time 47 secs

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1 MOLETYPE TYPE: peptide
2 FEATURE:
3 NAME/KEY: Modified-site
4 LOCATION: 13
5 OTHER INFORMATION: /product: "OTHER"
6 OTHER INFORMATION: /note: "Xaa - Ile, Met, Thr, Asn, Lys,
7 OTHER INFORMATION: Ser or Arg"
8 FEATURE:
9 NAME/KEY: Modified-site
10 LOCATION: 14
11 OTHER INFORMATION: /product: "OTHER"
12 OTHER INFORMATION: /note: "Xaa - Cys, Arg, Ser or Gly"
13 US 09-214-913-38
14
15 Query Match 44 68; Score 37, DB 8, Length 14;
16 Best Local Similarity 87.5%; P-adj 90.267
17 Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0
18
19 QY 5 PPKKKKKK 12
20 DB 2 PPKKKKKK 9
21
22 RESULT 2
23 US-10-119-714-7
24 Sequence 7, Application US/10119714
25 Patent No. US6000133467A1
26 GENERAL INFORMATION:
27 APPLICANT: PETIT, CHRISTINE
28 APPLICANT: COUSSEY, YVES; MACIA
29 APPLICANT: HARDELIN, JEAN PIERRE
30 APPLICANT: SARAILH, CATHERINE
31 APPLICANT: EUGON, GENEVIEVE
32 APPLICANT: LEGOUIC, RENAUD
33 APPLICANT: AETOUIN, OLIVIER
34 APPLICANT: MAZIE, JEAN-CLAUDE
35 TITLE OF INVENTION: THERAPEUTIC COMPOSITION COMPRISING FAL PROTEIN AND USE
36 TITLE OF INVENTION: OF THE FAL PROTEIN FOR THE TREATMENT OF FETAL, PERIL,
37 TITLE OF INVENTION: REFUSAL AND REPAIR INJURY
38 FILE REFERENCE: 0680-0151-OXECT
39 CURRENT APPLICATION NUMBER: 03/10/119,714
40 PRIOR FILING DATE: 2002 04-11
41 PRIOR FILING DATE: 1999 09 02
42 NUMBER OF SEQ ID NOS: 9
43 SOFTWARE: PASCALIN Ver. 2.1
44 SEQ ID NO: 7
45 LENGTH: 16
46 TYPE: PRT
47 ORGANISM: Artificial Sequence
48 FEATURE:
49 OTHER INFORMATION: Description of Artificial Sequence:peptide
50 US-10-119-714-7
51
52 Query Match 42.01; Score 25, DB 12, Length 16,
53 Best Local Similarity 54.53; P-adj 70.72
54 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
55
56 QY 5 PPKKKKKK 16
57 DB 4 PPKKKKKK 14
58
59 RESULT 3
60 US-09-214-913-38
61 Sequence 7, Application US/0909346A
62 Patent No. US6000133467A1
63 GENERAL INFORMATION:
64 APPLICANT: PETIT, CHRISTINE
65 APPLICANT: COUSSEY, YVES; MACIA
66 TITLE OF INVENTION: THERAPEUTIC COMPOSITION COMPRISING FAL PROTEIN AND USE
67 TITLE OF INVENTION: OF THE FAL PROTEIN FOR THE TREATMENT OF FETAL, PERIL,
68 TITLE OF INVENTION: REFUSAL AND REPAIR INJURY
69 FILE REFERENCE: 0680-0151-OXECT
70 CURRENT APPLICATION NUMBER: 03/10/119,714
71 PRIOR FILING DATE: 2002 04-11
72 PRIOR FILING DATE: 1999 09 02
73 NUMBER OF SEQ ID NOS: 9
74 SOFTWARE: PASCALIN Ver. 2.1
75 SEQ ID NO: 7
76 LENGTH: 16
77 TYPE: PRT
78 ORGANISM: Artificial Sequence
79 FEATURE:
80 OTHER INFORMATION: Description of Artificial Sequence:peptide
81 US-10-119-714-7
82
83 Query Match 42.01; Score 25, DB 12, Length 16,
84 Best Local Similarity 54.53; P-adj 70.72
85 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
86
87 QY 5 PPKKKKKK 16
88 DB 4 PPKKKKKK 14
89
90 RESULT 3
91 US-09-214-913-38
92 Sequence 7, Application US/0909346A
93 Patent No. US6000133467A1
94 GENERAL INFORMATION:
95 APPLICANT: PETIT, CHRISTINE
96 APPLICANT: COUSSEY, YVES; MACIA
97 TITLE OF INVENTION: THERAPEUTIC COMPOSITION COMPRISING FAL PROTEIN AND USE
98 TITLE OF INVENTION: OF THE FAL PROTEIN FOR THE TREATMENT OF FETAL, PERIL,
99 TITLE OF INVENTION: REFUSAL AND REPAIR INJURY
100 FILE REFERENCE: 0680-0151-OXECT
101 CURRENT APPLICATION NUMBER: 03/10/119,714
102 PRIOR FILING DATE: 2002 04-11
103 PRIOR FILING DATE: 1999 09 02
104 NUMBER OF SEQ ID NOS: 9
105 SOFTWARE: PASCALIN Ver. 2.1
106 SEQ ID NO: 7
107 LENGTH: 16
108 TYPE: PRT
109 ORGANISM: Artificial Sequence
110 FEATURE:
111 OTHER INFORMATION: Description of Artificial Sequence:peptide
112 US-10-119-714-7
113
114 Query Match 41 68; Score 34, DB 10; Length 10;
115 Best Local Similarity 76.53; P-adj 90.267
116 Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
117
118 QY 4 PPKKKKKK 13
119 DB 1 PPKKKKKK 10
120
121 RESULT 4
122 US-09-214-913-38
123 Sequence 44, Application US/0909346A
124 Patent No. US6000133467A1
125 GENERAL INFORMATION:
126 APPLICANT: Smith, Louis C.
127 Sparrow, James T.
128 Hauer, Jochen
129 Mims, Martha P.
130 TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
131 WATER-SOLUBLE DELIVERY
132 NUMBER OF SEQUENCES: 139
133 CORRESPONDENCE ADDRESS:
134 ADDRESSEE: Lynn A. Lyon
135 STREET: 633 West Fifth Street
136 Suite 4700
137 CITY: Los Angeles
138 STATE: California
139 COUNTRY: U.S.A.
140 ZIP: 90071-2056
141 COMPUTER READABLE FORM: Diskette, 1.44 Mb
142 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
143 storage
144 COMPUTER: IBM Compatible
145 OPERATING SYSTEM: IBM PC DOS 5.0
146 SOFTWARE: Word Perfect 6.1
147 CURRENT APPLICATION DATA:
148 APPLICATION NUMBER: US/09/09346A
149 FILING DATE: 10 Mar 2001
150 CLASSIFICATION:
151 PRIORITY APPLICATION DATA:
152 APPLICATION NUMBER: 09/564,043

```

```

1 ADDRESSEE: Rodman, Gifford & Costigan
2 STREET: 1185 Avenue of the Americas
3 CITY: New York
4 STATE: New York
5 COUNTRY: USA
6 ZIP: 10036
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
9 COMPUTER: IBM PS/2
10 OPERATING SYSTEM: DOS
11 SOFTWARE: Word Perfect 6.1
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: US/09/09346A
14 FILING DATE: July 29, 1998
15 CLASSIFICATION: 424
16 PRIORITY APPLICATION DATA:
17 APPLICATION NUMBER:
18 FILING DATE:
19 ATTORNEY/AGENT INFORMATION:
20 NAME: Costigan, James V.
21 REGISTRATION NUMBER: 25,669
22 REFERENCE/DOCKET NUMBER: 575-008
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: (212) 202-8989
25 TELEFAX: (212) 202-8989
26 INFORMATION FOR SEQ ID NO: 1:
27 SEQUENCE CHARACTERISTICS:
28 LENGTH: 10 amino acids
29 TYPE: amino acid
30 TOPOLOGY: circular
31 US 09-214-913-38
32
33 Query Match 41 68; Score 34, DB 10; Length 10;
34 Best Local Similarity 76.53; P-adj 90.267
35 Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
36
37 QY 4 PPKKKKKK 13
38 DB 1 PPKKKKKK 10
39
40 RESULT 4
41 US-09-214-913-38
42 Sequence 44, Application US/0909346A
43 Patent No. US6000133467A1
44 GENERAL INFORMATION:
45 APPLICANT: Smith, Louis C.
46 Sparrow, James T.
47 Hauer, Jochen
48 Mims, Martha P.
49 TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
50 WATER-SOLUBLE DELIVERY
51 NUMBER OF SEQUENCES: 139
52 CORRESPONDENCE ADDRESS:
53 ADDRESSEE: Lynn A. Lyon
54 STREET: 633 West Fifth Street
55 Suite 4700
56 CITY: Los Angeles
57 STATE: California
58 COUNTRY: U.S.A.
59 ZIP: 90071-2056
60 COMPUTER READABLE FORM: Diskette, 1.44 Mb
61 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
62 storage
63 COMPUTER: IBM Compatible
64 OPERATING SYSTEM: IBM PC DOS 5.0
65 SOFTWARE: Word Perfect 6.1
66 CURRENT APPLICATION DATA:
67 APPLICATION NUMBER: US/09/09346A
68 FILING DATE: 10 Mar 2001
69 CLASSIFICATION:
70 PRIORITY APPLICATION DATA:
71 APPLICATION NUMBER: 09/564,043

```

UNKNOWN
NAME: Richard J.
NUMBER: 12,327
REGISTRATION NUMBER: 217/194
REFERENCE: 443 1600
SEQUENCE: 443 443

NAME: 443
REFERENCE: 443
SEQUENCE: 443
REFERENCE: 443
SEQUENCE: 443

NAME: "Xaa" status : any naturally
REF: 443 443

US SEQ ID NO: 443

Score: 443 12 34 Score: 123
Pred. No: 75
Matches: 7 Mismatches: 0 Gaps: 0

US-09-805-301-7

NAME: James T.
REFERENCE: 443
SEQUENCE: 443
REFERENCE: 443
SEQUENCE: 443

US-09-805-301-7

NAME: 443
REFERENCE: 443
SEQUENCE: 443
REFERENCE: 443
SEQUENCE: 443

US-09-805-301-7

NAME: 443
REFERENCE: 443
SEQUENCE: 443
REFERENCE: 443
SEQUENCE: 443

INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-09-805-301-100

Query Match 41.8% Score: 443 12 34 Length: 123
Best Local Similarity 70.8% Pred. No: 75
Matches: 7 Conservative 0 Mismatches: 0 Gaps: 0

QY 4 KPSKPKKKKK 13
DB 1 KKKKKKKKK 10

RESULT 6

US-09-805-301-7
Sequence 7, Application US/09805301
Patent No. US20020173456A1

GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
Sparrow, James T.
Hauer, Jochen
Mrs. Martha P.

TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 6.0
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/805,301
FILING DATE: 12-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/584,043
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warburton, Richard C.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 217/194
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-805-301-7

Query Match 41.8% Score: 443 12 34 Length: 123
Best Local Similarity 70.8% Pred. No: 75
Matches: 7 Conservative 0 Mismatches: 0 Gaps: 0

CY 4 KPSKPKPKK 13
| | | | |
DB 1 KPSKPKPKK 10

RESULT 7

US-09-805-301-45
? Sequence 45, Application US/09805301
? Patent No. US20020173456A1

GENERAL INFORMATION:

APPLICANT: Smith, Louis C.
Sparrow, James T.
Hauer, Jochen

Mims, Martha P.

TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
MACROMOLECULE DELIVERY

NUMBER OF SEQUENCES: 139

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071 2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 6.0

SOFTWARE: Word Perfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/805,301

FILING DATE: 12 Mar 2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/804,042

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE: PCT NUMBER: 11/189

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

OTHER INFORMATION: "Xaa" stands for any naturally

occurring amino acid and

analogues thereof.

SEQUENCE DESCRIPTION: SEQ ID NO: 45:

US-09-805-301-45

Cy 4 KPSKPKPKK 13

| | | | |

DB 1 KPSKPKPKK 10

RESULT 8

US-09-805-301-101

? Sequence 101, Application US/09805301

? Patent No. US20020173456A1

GENERAL INFORMATION:

APPLICANT: Smith, Louis C.
Sparrow, James T.
Hauer, Jochen

Mims, Martha P.

TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
MACROMOLECULE DELIVERY

NUMBER OF SEQUENCES: 139

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071 2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 6.0

SOFTWARE: Word Perfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/805,301

FILING DATE: 12 Mar 2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/584,043

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE: PCT NUMBER: 11/189

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 101:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 101:

US-09-805-301-101

Cy 4 KPSKPKPKK 13

| | | | |

DB 1 KPSKPKPKK 10

RESULT 9

US-09-805-301-8

? Sequence 8, Application US/09805301

? Patent No. US20020173456A1

GENERAL INFORMATION:

APPLICANT: Smith, Louis C.

Sparrow, James T.

Hauer, Jochen

Mims, Martha P.

TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
MACROMOLECULE DELIVERY

NUMBER OF SEQUENCES: 139

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

Suite 4700

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/584,043
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 12,127
REFERENCE/DOCKET NUMBER: 217/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 483-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: "Xaa" stands for any naturally
occurring amino acid and
analogues thereof.
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-09-805-301-46
Query Match 41.0%; Score 34; DP 0; Length 14;
Best Local Similarity 70.0%; Pred. No. 96;
Matches 7; Conservative 0; Mismatches 3; Gaps 0;
QY 4 KPSKSKKKK 13
DP 1 KKKKKKKK 10
RESULT 11
US-09-805-301-102
Sequence 102, Application Us/09805101;
Patent No. 5220221/73456A1
GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
Hauer, James T.
Mims, Martha D.
TITLE OF INVENTION: LIPIDIC PEPTIDES FOR
MACROMOLECULE DELIVERY
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 West Fifth Street
Suite 4720
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 4.0
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09805,101
FILING DATE: 12-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/584,043
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 12,127
REFERENCE/DOCKET NUMBER: 217/149
TELECOMMUNICATION INFORMATION:

US-09-805-301-102
Sequence 102, Application Us/09805101;
Patent No. 5220221/73456A1
GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
Hauer, James T.
Mims, Martha D.
TITLE OF INVENTION: LIPIDIC PEPTIDES FOR
MACROMOLECULE DELIVERY
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 West Fifth Street
Suite 4720
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 4.0
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09805,101
FILING DATE: 12-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/584,043
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 12,127
REFERENCE/DOCKET NUMBER: 217/149
TELECOMMUNICATION INFORMATION:

US-09-805-301-102
Sequence 102, Application Us/09805101;
Patent No. 5220221/73456A1
GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
Hauer, James T.
Mims, Martha D.
TITLE OF INVENTION: LIPIDIC PEPTIDES FOR
MACROMOLECULE DELIVERY
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 West Fifth Street
Suite 4720
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 4.0
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09805,101
FILING DATE: 12-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/584,043
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 12,127
REFERENCE/DOCKET NUMBER: 217/149
TELECOMMUNICATION INFORMATION:

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TELEPHONE (213) 499-1000
TELEFAX (213) 955-0440
TELEX 67-3510
INFORMATION FOR SEQ ID NO: 102.
SEQUENCE CHARACTERISTICS:
  LENGTH: 14 amino acids
  TYPE: amino acid
  STRANDEDNESS: single
  TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 102.
US-09-093-067-102

Query Match
Best Local Similarity 70.0%, Score 29, Indels 3, Mismatches 0, Gaps 0,
Matches 7, Conservative 0, Mismatches 0, Gaps 0,

QY 4 KPSPPKYYK 13
DB 1 KKKKKKKK 10

RESULT 12
US-09-093-067-1
  Query Match
  Best Local Similarity 70.0%, Score 29, Indels 3, Mismatches 0, Gaps 0,
  Matches 7, Conservative 0, Mismatches 0, Gaps 0,
  GENERAL INFORMATION:
  APPLICANT: INOUE, AVO
  APPLICANT: SHIMIZU, Katsuhiko
  APPLICANT: CEDA, Takaya
  TITLE OF INVENTION: Processes for Producing Peptides By Using In Vitro
  TITLE OF INVENTION: Transcription/Translation System
  FILE REFERENCE: 1752-011P
  CURRENT APPLICATION NUMBER: US/09/093,067
  CURRENT FILING DATE: 2001-10-23
  PRIOR APPLICATION NUMBER: JP 294795/2001
  PRIOR FILING DATE: 2001-09-26
  PRIOR APPLICATION NUMBER: JP 227094/2001
  PRIOR FILING DATE: 2001-07-27
  PRIOR APPLICATION NUMBER: JP 231120/2001
  PRIOR FILING DATE: 2001-01-15
  PRIOR APPLICATION NUMBER: JP 401417/2000
  PRIOR FILING DATE: 2000-12-28
  NUMBER OF SEQ ID NOS: 6
  SOFTWARE: PatentIn version 3.1
  SEQ ID NO: 1
  LENGTH: 14
  TYPE: PRT
  ORGANISM: Bovine sp.
US-09-093-067-1

Query Match
Best Local Similarity 41.0%, Score 34, Indels 14, Length 14,
Matches 6, Conservative 2, Mismatches 2, Indels 0, Gaps 0,

QY 4 KPSPPKYYK 13
DB 5 QKKKKKKK 14

RESULT 13
US-09-805-301-9
  Query Match
  Best Local Similarity 60.0%, Score 34, Indels 14, Length 14,
  Matches 6, Conservative 2, Mismatches 2, Indels 0, Gaps 0,
  GENERAL INFORMATION:
  APPLICANT: Smith, Louis C.
  APPLICANT: Sparrow, James T.
  APPLICANT: Hauer, Jochen
  APPLICANT: Mims, Martha P.
  TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
  MACROMOLECULE DELIVERY
  NUMBER OF SEQUENCES: 139
  CORRESPONDENCE ADDRESS:
  ADDRESS: Lyon & Lyon
  STREET: 411 West Fifth Street
  CITY: Los Angeles
  STATE: California
  COUNTRY: U.S.A.
  ZIP: 90071-2066
  MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
  COMPUTER: IBM Compatible
  OPERATING SYSTEM: IBM PC DOS 6.0
  SOFTWARE: Word Perfect 6.1
  OFF-WARE: Word Perfect 6.1
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APPLICANT: Lyon & Lyon
STREET: 411 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM PC DOS 6.0
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: 08/584,043
  FILING DATE: 12 May 2001
  CLASSIFICATION: <Unknown>
  PRIORITY DATA:
  APPLICATION NUMBER: 08/584,043
  FILING DATE: <Unknown>
  ATTORNEY/AGENT INFORMATION:
  NAME: Warburg, Richard J.
  REGISTRATION NUMBER: 93,327
  REFERENCE/DOCKET NUMBER: 210/189
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: (213) 499-1600
  TELEFAX: (213) 955-0440
  TELEX: 67-3510
  INFORMATION FOR SEQ ID NO: 9:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 15 amino acids
    TYPE: amino acid
    STRANDEDNESS: single
    TOPOLOGY: linear
    MOLECULE TYPE: peptide
  SEQUENCE DESCRIPTION: SEQ ID NO: 9:
  US-09-093-301-9

Query Match
Best Local Similarity 70.0%, Score 34, Indels 14,
Matches 7, Conservative 0, Mismatches 3, Indels 0, Gaps 0,

QY 4 KPSPPKYYK 13
DB 1 KKKKKKKK 10

RESULT 14
US-09-805-301-47
  Query Match
  Best Local Similarity 60.0%, Score 34, Indels 14,
  Matches 7, Conservative 0, Mismatches 3, Indels 0, Gaps 0,
  GENERAL INFORMATION:
  APPLICANT: Smith, Louis C.
  APPLICANT: Sparrow, James T.
  APPLICANT: Hauer, Jochen
  APPLICANT: Mims, Martha P.
  TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
  MACROMOLECULE DELIVERY
  NUMBER OF SEQUENCES: 139
  CORRESPONDENCE ADDRESS:
  ADDRESS: Lyon & Lyon
  STREET: 411 West Fifth Street
  CITY: Los Angeles
  STATE: California
  COUNTRY: U.S.A.
  ZIP: 90071-2066
  MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
  COMPUTER: IBM Compatible
  OPERATING SYSTEM: IBM PC DOS 6.0
  SOFTWARE: Word Perfect 6.1
```


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28 34 41.0 15 4 US-08-584-043A-42 Sequence 42, App
29 34 41.0 15 4 US-08-584-043A-43 Sequence 43, App
30 34 41.0 15 4 US-08-584-043A-44 Sequence 44, App
31 34 41.0 15 4 US-08-584-043A-45 Sequence 45, App
32 34 41.0 15 4 US-08-584-043A-46 Sequence 46, App
33 34 41.0 15 4 US-08-584-043A-47 Sequence 47, App
34 34 41.0 15 4 US-08-584-043A-48 Sequence 48, App
35 34 41.0 15 4 US-08-584-043A-49 Sequence 49, App
36 34 41.0 15 4 US-08-584-043A-50 Sequence 50, App
37 34 41.0 15 4 US-08-584-043A-51 Sequence 51, App
38 34 41.0 15 4 US-08-584-043A-52 Sequence 52, App
39 34 41.0 15 4 US-08-584-043A-53 Sequence 53, App
40 34 41.0 15 4 US-08-584-043A-54 Sequence 54, App
41 34 41.0 15 4 US-08-584-043A-55 Sequence 55, App
42 34 41.0 15 4 US-08-584-043A-56 Sequence 56, App
43 34 41.0 15 4 US-08-584-043A-57 Sequence 57, App
44 34 41.0 15 4 US-08-584-043A-58 Sequence 58, App
45 34 41.0 15 4 US-08-584-043A-59 Sequence 59, App

28 34 41.0 15 4 US-08-584-043A-42 Sequence 42, App
29 34 41.0 15 4 US-08-584-043A-43 Sequence 43, App
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31 34 41.0 15 4 US-08-584-043A-45 Sequence 45, App
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33 34 41.0 15 4 US-08-584-043A-47 Sequence 47, App
34 34 41.0 15 4 US-08-584-043A-48 Sequence 48, App
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37 34 41.0 15 4 US-08-584-043A-51 Sequence 51, App
38 34 41.0 15 4 US-08-584-043A-52 Sequence 52, App
39 34 41.0 15 4 US-08-584-043A-53 Sequence 53, App
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42 34 41.0 15 4 US-08-584-043A-56 Sequence 56, App
43 34 41.0 15 4 US-08-584-043A-57 Sequence 57, App
44 34 41.0 15 4 US-08-584-043A-58 Sequence 58, App
45 34 41.0 15 4 US-08-584-043A-59 Sequence 59, App

ALIGNMENTS

RESULT 1
517861-17
; Patent No. 517861
; APPLICANT: VERGARA, ULISES; RUIZ, ANDRES; PERREIRA, ARTURO;
; MUEGENWEIS, RUTH S.; KESSENWEIG, VICTOR N.
; TITLE OF INVENTION: CROSS REACTIVE AND PROTECTIVE EPITOPES
; OF CIRCUMFEROZITE PROTEINS
; NUMBER OF SEQUENCES: 18
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,241
; FILING DATE: 22 JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 115,634
; FILING DATE: 26 OCT-1987
; APPLICATION NUMBER: 649,903
; FILING DATE: 12-SEP-1984
; SEQ ID NO: 17
; LENGTH: 13
517861-17

ALIGNMENTS

Query Match 49.4%; Score 41; DE 6; Length 13;
Best Local Similarity 53.8%; Pred. No. 5; 4; Matches 8; Gaps 1;
Matches 7; Conservative 2; Mismatches 4; Gaps 1;
QV 4 PPSPPPPPPPPPP 16
DI 1 PPSPPPPPPPPPP 13
RESULT 2
US-08-469-582-15
; Sequence 15, Application US/08469592
; Patent No. 567576
; GENERAL INFORMATION
; APPLICANT: Dickerson, Kenneth T.
; APPLICANT: Glass, James R.
; APPLICANT: Liu, Lin-Shu
; APPLICANT: Polarek, James W.
; APPLICANT: Craig, William S.
; APPLICANT: Mullen, Daniel G.
; APPLICANT: Cheng, Soan
; TITLE OF INVENTION: Immobilization of Peptides to
; HYALURONIC ACID
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4300 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA

Query Match 49.4%; Score 41; DE 6; Length 13;
Best Local Similarity 53.8%; Pred. No. 5; 4; Matches 8; Gaps 1;
Matches 7; Conservative 2; Mismatches 4; Gaps 1;
QV 4 PPSPPPPPPPPPP 16
DI 1 PPSPPPPPPPPPP 13

Query Match 49.4%; Score 41; DE 6; Length 13;
Best Local Similarity 53.8%; Pred. No. 5; 4; Matches 8; Gaps 1;
Matches 7; Conservative 2; Mismatches 4; Gaps 1;
QV 4 PPSPPPPPPPPPP 16
DI 1 PPSPPPPPPPPPP 13

28 34 41.0 15 4 US-08-584-043A-42 Sequence 42, App
29 34 41.0 15 4 US-08-584-043A-43 Sequence 43, App
30 34 41.0 15 4 US-08-584-043A-44 Sequence 44, App
31 34 41.0 15 4 US-08-584-043A-45 Sequence 45, App
32 34 41.0 15 4 US-08-584-043A-46 Sequence 46, App
33 34 41.0 15 4 US-08-584-043A-47 Sequence 47, App
34 34 41.0 15 4 US-08-584-043A-48 Sequence 48, App
35 34 41.0 15 4 US-08-584-043A-49 Sequence 49, App
36 34 41.0 15 4 US-08-584-043A-50 Sequence 50, App
37 34 41.0 15 4 US-08-584-043A-51 Sequence 51, App
38 34 41.0 15 4 US-08-584-043A-52 Sequence 52, App
39 34 41.0 15 4 US-08-584-043A-53 Sequence 53, App
40 34 41.0 15 4 US-08-584-043A-54 Sequence 54, App
41 34 41.0 15 4 US-08-584-043A-55 Sequence 55, App
42 34 41.0 15 4 US-08-584-043A-56 Sequence 56, App
43 34 41.0 15 4 US-08-584-043A-57 Sequence 57, App
44 34 41.0 15 4 US-08-584-043A-58 Sequence 58, App
45 34 41.0 15 4 US-08-584-043A-59 Sequence 59, App

28 34 41.0 15 4 US-08-584-043A-42 Sequence 42, App
29 34 41.0 15 4 US-08-584-043A-43 Sequence 43, App
30 34 41.0 15 4 US-08-584-043A-44 Sequence 44, App
31 34 41.0 15 4 US-08-584-043A-45 Sequence 45, App
32 34 41.0 15 4 US-08-584-043A-46 Sequence 46, App
33 34 41.0 15 4 US-08-584-043A-47 Sequence 47, App
34 34 41.0 15 4 US-08-584-043A-48 Sequence 48, App
35 34 41.0 15 4 US-08-584-043A-49 Sequence 49, App
36 34 41.0 15 4 US-08-584-043A-50 Sequence 50, App
37 34 41.0 15 4 US-08-584-043A-51 Sequence 51, App
38 34 41.0 15 4 US-08-584-043A-52 Sequence 52, App
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41 34 41.0 15 4 US-08-584-043A-55 Sequence 55, App
42 34 41.0 15 4 US-08-584-043A-56 Sequence 56, App
43 34 41.0 15 4 US-08-584-043A-57 Sequence 57, App
44 34 41.0 15 4 US-08-584-043A-58 Sequence 58, App
45 34 41.0 15 4 US-08-584-043A-59 Sequence 59, App

SUMMARIES

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equal to the score of the result being printed,
ysis of the total score distribution.

28 34 41.0 15 4 US-08-584-043A-42 Sequence 42, App
29 34 41.0 15 4 US-08-584-043A-43 Sequence 43, App
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32 34 41.0 15 4 US-08-584-043A-46 Sequence 46, App
33 34 41.0 15 4 US-08-584-043A-47 Sequence 47, App
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36 34 41.0 15 4 US-08-584-043A-50 Sequence 50, App
37 34 41.0 15 4 US-08-584-043A-51 Sequence 51, App
38 34 41.0 15 4 US-08-584-043A-52 Sequence 52, App
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42 34 41.0 15 4 US-08-584-043A-56 Sequence 56, App
43 34 41.0 15 4 US-08-584-043A-57 Sequence 57, App
44 34 41.0 15 4 US-08-584-043A-58 Sequence 58, App
45 34 41.0 15 4 US-08-584-043A-59 Sequence 59, App

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213. 02102
COMPUTER READABLE FORM.
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/469,582
FILING DATE: 05-JUN-1995
CLASSIFICATION: 510
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/469,513
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Kathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1550
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8901
TELEFAX: (619) 535-8919
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-469-582 15

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Query Match 42.44, Score 25, PP 1, Length 13,
Best Local Similarity 82.54, Pct ID 33,
Matches 7, Conservative 1, Mismatches 5, Indels 0, Gaps 0,

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QY 1 GGGSESPKPPK 13
DE 1 GGGSESPKPPK 13

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RESULT 3
US-08-105-904B-21
Sequence 9, Application US/09105904P
Patent No. 6001364
GENERAL INFORMATION:
APPLICANT: Rose, Keith
APPLICANT: Offord, Robin
TITLE OF INVENTION: HETERO-POLYMER COMPOUNDS AND THEIR
PREPARATION BY PARALLEL ASSEMBLY
TITLE OF INVENTION: HETERO-POLYMER COMPOUNDS AND THEIR
PREPARATION BY PARALLEL ASSEMBLY
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSER: Colley Godward Castro Huddleston & Tatum
STREET: 5 Palo Alto Square, 3000 El Camino Real
CITY: Palo Alto
STATE: California
COUNTRY: U.S.A.
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/469,582
FILING DATE: 31-AUG-1993
CLASSIFICATION: 421
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/469,504
FILING DATE: 05-MAY-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Neely, Richard L.
REGISTRATION NUMBER: 30,093
REFERENCE/DOCKET NUMBER: LA20 001/0203
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 957-0663
TELEFAX: (415) 957-0663

```

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TELEX: 330016 ColleyPA
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: peptide
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: Cys-Gly
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: Lys-Gly
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: Lys-Gly
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: Lys-Gly
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: Lys-Gly
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: Lys-Gly
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: Lys-Gly
FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: Lys-Gly
US-08-105-904B-9

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Query Match 42.24, Score 25, PP 3, Length 11,
Best Local Similarity 82.54, Pct ID 33,
Matches 7, Conservative 1, Mismatches 0, Indels 0, Gaps 0,

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QY 9 KKKKKKPG 15
DE 4 KKKKKKPG 11

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RESULT 4
US-09-105-904B-21
Sequence 21, Application US/09105904P
Patent No. 6001364
GENERAL INFORMATION:
APPLICANT: Rose, Keith
APPLICANT: Offord, Robin
TITLE OF INVENTION: HETERO-POLYMER COMPOUNDS AND THEIR
PREPARATION BY PARALLEL ASSEMBLY
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSER: Colley Godward Castro Huddleston & Tatum
STREET: 5 Palo Alto Square, 3000 El Camino Real
CITY: Palo Alto
STATE: California
COUNTRY: U.S.A.
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

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Best Local Similarity 87.58; Pred. No. 33;
Matches 7, Conservative 6, Mismatches 1, Indels 3, Gaps 0;

CY 9 KKKKKKGG 15
| | | | |
DB 4 KKKKKKGG 11

RESULT 6

US-08-114-877A-14
Sequence 14, Application US/08114877A

Patent No. 674513

GENERAL INFORMATION:

APPLICANT: Rose, Keith

APPLICANT: Clifford, Robin

TITLE OF INVENTION: HMM-BASED POLYMERASE COMPOSITIONS AND THEIR

USE IN SEQUENCING

TITLE OF INVENTION: PREPARATION BY ENZYME ASSEMBLY

NUMBER OF SEQUENCES: 15

CLASSIFICATION: A61K

ADDRESS: Cooley Goddard Castro Huddleson & Tatum

STREET: 5 Palo Alto Square

CITY: Palo Alto

STATE: California

COUNTRY: U.S.A.

ZIP: 94036

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 02/09/114,877A

FILING DATE: 31-AUG-1993

CLASSIFICATION: A61K

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 02/057,694

FILING DATE: 05-MAY-1993

CLASSIFICATION: A61K

ATTORNEY/AGENT INFORMATION:

NAME: Nealey, Richard L.

REGISTRATION NUMBER: 30,092

REFERENCE/DOCKET NUMBER: ABIC 001/0103

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 843 5070

TELEFAX: (415) 857-0663

TELEX: 380816 CooleySA

INFORMATION FOR SEQ 13, NEA 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

TOPOLGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: Modified-site

LOCATION: 4

OTHER INFORMATION: Lys BCC

FEATURE:

NAME/KEY: Modified-site

LOCATION: 6

OTHER INFORMATION: Lys BCC

FEATURE:

NAME/KEY: Modified-site

LOCATION: 6

OTHER INFORMATION: Lys BCC

FEATURE:

NAME/KEY: Modified-site

LOCATION: 7

OTHER INFORMATION: Lys BCC

FEATURE:

NAME/KEY: Modified-site

LOCATION: 8

OTHER INFORMATION: Lys BCC

FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: Lys-BCC
FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: Lys-BCC
FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: Lys-BCC
US-08-114-877A-14

Query Match 42.28, Score 35, DB 4, Length 11;
Best Local Similarity 67.67, Pred. No. 33;
Matches 7, Conservative 6, Mismatches 1, Indels 3, Gaps 0;

CY 9 KKKKKKGG 15
| | | | |
DB 4 KKKKKKGG 11

RESULT 7

5171843-11

Patent No. 5171843

APPLICANT: NUSSENZWEIG, VICTOR

TITLE OF INVENTION: IMMUNOGENIC POLYPEPTIDE AND METHOD FOR

PURIFYING IT

NUMBER OF SEQUENCES: 13

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 02/03/175,112

FILING DATE: 30-MAR-1988

CLASSIFICATION: A61K

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 754,645

FILING DATE: 9-JUL-1985

CLASSIFICATION: A61K

FILING DATE: 26-SEP-1989

APPLICATION NUMBER: 649,923

FILING DATE: 12-SEP-1984

SEQ ID NO:11:

LENGTH: 15

5171843-11

Query Match

Best Local Similarity 42.28, Score 35, DB 4, Length 15;

Matches 6, Conservative 3, Mismatches 3, Indels 3, Gaps 0;

CY 4 KKKKKKKKKGG 15
| | | | |
DB 4 KKKKKKKKKGG 15

RESULT 8

US-08-097-810E-1

Sequence 1, Application US/08049830E

Patent No. 676211

GENERAL INFORMATION:

APPLICANT: Parvo, Massimo

TITLE OF INVENTION: Peptides For Modulating The

Activity of IL-1A

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESS: Hedman, Gibson & Costigan, P.C.

STREET: 1195 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB Storage

COMPUTER: IBM PS/2

OPERATING SYSTEM: DOS

Query Match
Best Local Similarity 70.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatched 1; Inp. 8; Outp. 10

QV 4 KPSKYYK 13
| | | | |
DB 1 KPSKYYK 10

US-08-373-190-54
Sequence 54, Application US/09373190
Patent No. 5851829
GENERAL INFORMATION:
APPLICANT: MARASCO, WAYNE
TITLE OF INVENTION: METHOD OF INTRA-CELLULAR KINININ-
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CURRAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,190
FILING DATE: 17-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06788
FILING DATE: 16-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 41956 PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: STRE UR 2002
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N terminal
ORIGINAL SOURCE:
US-08-373-190-54

Query Match
Best Local Similarity 41.0%; Score 34; DB 2; Length 10;
Matches 6; Conservative 2; Mismatched 1; Inp. 8; Outp. 10

QV 5 SPKYYK 13
| | | | |
DB 1 TPPEK 9

US-08-438-190A-54
Sequence 54, Application US/08438190A
Patent No. 5965371
GENERAL INFORMATION:
APPLICANT: MARASCO, WAYNE
TITLE OF INVENTION: METHOD OF INTRA-CELLULAR KINININ-
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CURRAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,190A
FILING DATE: 17-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06788
FILING DATE: 16-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 41956 PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: STRE UR 2002
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N terminal
ORIGINAL SOURCE:
US-08-438-190A-54

Query Match
Best Local Similarity 66.7%; Pred. No. 42;
Matches 6; Conservative 2; Mismatched 1; Inp. 8; Outp. 10

QV 5 SPKYYK 13
| | | | |
DB 1 TPPEK 9

US-08-438-190A-54
Sequence 54, Application US/08438190A
Patent No. 5965371
GENERAL INFORMATION:
APPLICANT: MARASCO, WAYNE
TITLE OF INVENTION: METHOD OF INTRA-CELLULAR KINININ-
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CURRAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,190A
FILING DATE: 17-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06788
FILING DATE: 16-JUL-1993
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N terminal
ORIGINAL SOURCE:
US-08-438-190A-54

Query Match
Best Local Similarity 41.0%; Score 34; DB 2; Length 10;
Matches 6; Conservative 2; Mismatched 1; Inp. 8; Outp. 10

QV 5 SPKYYK 13
| | | | |
DB 1 TPPEK 9

US-08-438-190A-54
Sequence 54, Application US/08438190A
Patent No. 5965371
GENERAL INFORMATION:
APPLICANT: MARASCO, WAYNE
TITLE OF INVENTION: METHOD OF INTRA-CELLULAR KINININ-
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
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US-08-438-190A-54

Query Match
Best Local Similarity 41.0%; Score 34; DB 2; Length 10;
Matches 6; Conservative 2; Mismatched 1; Inp. 8; Outp. 10

QV 5 SPKYYK 13
| | | | |
DB 1 TPPEK 9

US-08-438-190A-54
Sequence 54, Application US/08438190A
Patent No. 5965371
GENERAL INFORMATION:
APPLICANT: MARASCO, WAYNE
TITLE OF INVENTION: METHOD OF INTRA-CELLULAR KINININ-
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N terminal
ORIGINAL SOURCE:
US-08-438-190A-54

Query Match
Best Local Similarity 41.0%; Score 34; DB 2; Length 10;
Matches 6; Conservative 2; Mismatched 1; Inp. 8; Outp. 10

QV 5 SPKYYK 13
| | | | |
DB 1 TPPEK 9

US-08-438-190A-54
Sequence 54, Application US/08438190A
Patent No. 5965371
GENERAL INFORMATION:
APPLICANT: MARASCO, WAYNE
TITLE OF INVENTION: METHOD OF INTRA-CELLULAR KINININ-
NUMBER OF SEQUENCES: 79
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STATE: MA
COUNTRY: US
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SOFTWARE: FASTSEQ Version 1.5
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FILING DATE: 17-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06788
FILING DATE: 16-JUL-1993
ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: 41956 PCT-US
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N terminal
ORIGINAL SOURCE:
US-08-438-190A-54

Query Match
Best Local Similarity 41.0%; Score 34; DB 2; Length 10;
Matches 6; Conservative 2; Mismatched 1; Inp. 8; Outp. 10

QV 5 SPKYYK 13
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DB 1 TPPEK 9

US-08-438-190A-54
Sequence 54, Application US/08438190A
Patent No. 5965371
GENERAL INFORMATION:
APPLICANT: MARASCO, WAYNE
TITLE OF INVENTION: METHOD OF INTRA-CELLULAR KINININ-
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TELEFAX: 617-523-6440
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INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N terminal
ORIGINAL SOURCE:
US-08-438-190A-54

LENGTH: 11 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1
OTHER INFORMATION: /label= Ac-
NAME/KEY: Peptide
LOCATION: 11
OTHER INFORMATION: /label= -NH2
US-07-694-983-15
Query Match 41.08; Score 34; DR 1; Length 11;
Best Local Similarity 70.0%; Pred: No; 46;
Matches 7; Mismatched 1; Mismatched 1; Gaps 0;

CY 4 KSPKPKPKPK 11
Db 2 KSPKPKPKPK 11

Search completed: March 3, 2003, 06:47:21
Job time : 16.6667 secs

EX: 11 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1
OTHER INFORMATION: /label= Ac-
NAME/KEY: Peptide
LOCATION: 11
OTHER INFORMATION: /label= -NH2
US-07-694-983-15
Query Match 41.08; Score 34; DR 1; Length 11;
Best Local Similarity 70.0%; Pred: No; 46;
Matches 7; Mismatched 1; Mismatched 1; Gaps 0;

Query Match 41.08; Score 34; DR 1; Length 11;
Best Local Similarity 70.0%; Pred: No; 46;
Matches 7; Mismatched 1; Mismatched 1; Gaps 0;

Query Match 41.08; Score 34; DR 1; Length 11;
Best Local Similarity 70.0%; Pred: No; 46;
Matches 7; Mismatched 1; Mismatched 1; Gaps 0;

Query Match 41.08; Score 34; DR 1; Length 11;
Best Local Similarity 70.0%; Pred: No; 46;
Matches 7; Mismatched 1; Mismatched 1; Gaps 0;

Query Match 41.08; Score 34; DR 1; Length 11;
Best Local Similarity 70.0%; Pred: No; 46;
Matches 7; Mismatched 1; Mismatched 1; Gaps 0;

Query Match 41.08; Score 34; DR 1; Length 11;
Best Local Similarity 70.0%; Pred: No; 46;
Matches 7; Mismatched 1; Mismatched 1; Gaps 0;

Query Match 41.08; Score 34; DR 1; Length 11;
Best Local Similarity 70.0%; Pred: No; 46;
Matches 7; Mismatched 1; Mismatched 1; Gaps 0;

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A:Accession: B59326
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-20 <OBP>
 A:Note: amino terminal of the mature form
 C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 22-18, Score 34, DB 2, Length 20;
 Best Local Similarity 55.6%; Pred. No. 4.1e+03;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 TPKKKKKK 14
 |||||
 Db 8 SPKIKKPKF 16

RESULT 15

C39305
 neurotoxin Tx3 - spider (Phoneutria nigriventer) (fragment)
 C:Species: Phoneutria nigriventer
 C:Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #LAST_CHANGE 07-Feb-1997
 C:Accession: C39305
 R:Rezende Jr., L.; Cordeiro, M.N.; Oliveira, E.B.; Diniz, C.R.
 Toxicol 29, 1225-1233, 1991
 A:Title: Isolation of neurotoxic peptides from the venom of the 'armed' spider Phoneutria nigriventer
 A:Reference number: A39305; MIM-9216803; PM10-1801316
 A:Accession: C39305
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-19 <PEZ>
 C:Keywords: neurotoxin

Query Match 22-68; Score 21.5; DB 2; Length 19;
 Best Local Similarity 40.8%; Pred. No. 4.6e+03;
 Matches 6; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 4 NETPPPPPPPPSPKK 18
 |||||
 Db 6 NES-QKKNVKKKK 19

Search completed: March 3, 2003, 06:59:52
 Job time : 48 secs

AC P35451;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE 17 kDa milk gly protein (Fragment).
OS Bos taurus (Bovine).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC Bovidae; Bovinae; 205.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Milk;
FX MEDLINE=3338294, PubMed:9323368;
RA Soerensen E.S., Petersen T.E.;
RT "Purification and characterization of three proteins isolated from
the protease prone fraction of bovine milk";
RL J. Dairy Res. 60:189-197(1993).
CC -1- P1M: N-GLYCOSYLATED.
CC -1- SIMILARITY: TO CAMEL WHEY PROTEIN.
KW Glycoprotein; Milk.
FT NON TER 1 1
FT NON TER 20 20
SQ SEQUENCE 21 AA: 40AA-94 41-9029 (RC64);
Query Match 21.2% Score 22; DP 1; Length 1;
Best Local Similarity 41.9% Field No. 23603;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 PSNETPK 8
DB 5 PQSQNPK 11
RESULT 14
TL18 SPIOL
ID TL18 SPIOL STANDARD; PRT: 20 AA.
AC P42530;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Thylakoid lumenal 18 kDa protein (P18) (Fragment).
OS Spinacia oleracea (Spinach).
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicot;
CC Caryophyllales; Caryophyllales; Cistaceae; Spinacia.
OX NCBI_TaxID=4562;
RN [1]
RP SEQUENCE.
RC Kieselbach T., Pustot W., Schroeder W.P.;
RA Submitted (May 2001) to the SWISS PROT data bank.
CC -1- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
KW Chloroplast; Thylakoid.
FT NON TER 1 10
SQ SEQUENCE 40 AA: 2152 NW, 2202NW-4497NW (RC64);
Query Match 21.2% Score 22; DP 1; Length 1;
Best Local Similarity 44.4% Field No. 23603;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 3 SNETPKKK 11
DB 2 AETPQSK 10
RESULT 15
RL16_ACHLA
ID RL16_ACHLA STANDARD; PRT: 10 AA.
AC P29221;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE 50S ribosomal protein L16 (Fragment).

AC P35451;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE 17 kDa milk gly protein (Fragment).
OS Bos taurus (Bovine).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC Bovidae; Bovinae; 205.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Milk;
FX MEDLINE=3338294, PubMed:9323368;
RA Soerensen E.S., Petersen T.E.;
RT "Purification and characterization of three proteins isolated from
the protease prone fraction of bovine milk";
RL J. Dairy Res. 60:189-197(1993).
CC -1- P1M: N-GLYCOSYLATED.
CC -1- SIMILARITY: TO CAMEL WHEY PROTEIN.
KW Glycoprotein; Milk.
FT NON TER 1 1
FT NON TER 20 20
SQ SEQUENCE 21 AA: 40AA-94 41-9029 (RC64);
Query Match 21.2% Score 22; DP 1; Length 1;
Best Local Similarity 41.9% Field No. 23603;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 PSNETPK 8
DB 5 PQSQNPK 11
RESULT 14
TL18 SPIOL
ID TL18 SPIOL STANDARD; PRT: 20 AA.
AC P42530;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Thylakoid lumenal 18 kDa protein (P18) (Fragment).
OS Spinacia oleracea (Spinach).
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicot;
CC Caryophyllales; Caryophyllales; Cistaceae; Spinacia.
OX NCBI_TaxID=4562;
RN [1]
RP SEQUENCE.
RC Kieselbach T., Pustot W., Schroeder W.P.;
RA Submitted (May 2001) to the SWISS PROT data bank.
CC -1- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
KW Chloroplast; Thylakoid.
FT NON TER 1 10
SQ SEQUENCE 40 AA: 2152 NW, 2202NW-4497NW (RC64);
Query Match 21.2% Score 22; DP 1; Length 1;
Best Local Similarity 44.4% Field No. 23603;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 3 SNETPKKK 11
DB 2 AETPQSK 10
RESULT 15
RL16_ACHLA
ID RL16_ACHLA STANDARD; PRT: 10 AA.
AC P29221;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE 50S ribosomal protein L16 (Fragment).

```

SN RPLP
OS Achlepiasma laidlawii.
OC Bacteria; Firmicutes; Mollicutes; Achlepiasmatales;
OC Achlepiasmataceae; Achlepiasma.
OX NCBI_TaxID=2148;
RN (1)
RP SEQUENCE FROM N.A. PubMed:156679;
RX WFLINF 051666; PubMed:156679;
RA Lim P.O., Sears B.B.;
RT "Evolutionary relationships of a plant-pathogenic mycoplasma-like
RT organism and Achlepiasma laidlawii deduced from two ribosomal protein
RT gene sequences.";
RL J. Bacteriol. 174:2696-2611(1992).
RC -1- FUNCTION: THIS PROTEIN BINES DIRECTLY TO 23S RIBOSOMAL RNA AND IS
CC LOCATED AT THE A SITE OF THE PEPTIDYLTRANSFERASE CENTER
CC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE L16S FAMILY OF RIBOSOMAL PROTEINS.
CC This Swiss-Prot entry is copyright. It is included through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.ist-sib.ch/announcement/
CC or send an email to license@sib-sib.ch)
CC -----
DR EMBL: M74771; AAC21914.1; -
DR PIR: F41839;
DR InterPro: IPR01114; Ribosomal_L16.
DR PROSITE: PS00584; RIBOSOMAL_L16_1; PARTIAL.
DR PROSITE: PS00701; RIBOSOMAL_L16_2; PARTIAL.
KW Ribosomal protein, rRNA-binding.
PT NON_TER 10
SQ SEQUENCE 10 AA: 1324 MW: 83562.418424156 CR054;

```

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Query Match 20.81; Score 21; DP 17; length 10;
Best Local Similarity 57.18; Pred. No. 1.6e+03;
Matcher 4; Conservative 1; Mismatch 2; Indels 0; Gaps 0;

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QY 7 PPKKKYP 13
DB 4 PKRTYR 10

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Search completed: March 3, 2003, 06:56:38
Job time : 31 secs


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RC STRAIN=US6;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
DR EMBL; M44830; AAA45700.1; -.
DP InterPro; IPR002502; HCV_Capsid.
DR Pfam; PPO1543; HCV_capsid; 1.
FT NON_TER 13 -13
SQ SEQUENCE 13 AA; 1512 MW; 454F97E1A42F76A3 ETC64;

Query Match 27.9%; Score 29; DB 12; Length 13;
Best Local Similarity 45.5%; Pred. No. 7.5e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 SNETPQKKYK 13
Db 3 TNPQPKYKTP 13

RESULT 9
Q81789 PRELIMINARY; PRT; 13 AA.
AC O81789;
DT 01-NOV-1996 (TrEMBLrel. 01, Created);
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update);
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update);
DE Polyprotein (Fragment);
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DK11;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
DR EMBL; M44831; AAA45706.1; -.
DP InterPro; IPR002502; HCV_Capsid.
DR Pfam; PPO1543; HCV_capsid; 1.
FT NON_TER 13 -13
SQ SEQUENCE 13 AA; 1512 MW; 454F97E1A42F76A3 ETC64;

Query Match 27.9%; Score 29; DB 12; Length 13;
Best Local Similarity 45.5%; Pred. No. 7.5e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 SNETPQKKYK 13
Db 3 TNPQPKYKTP 13

RESULT 10
Q81791 PRELIMINARY; PRT; 13 AA.
AC O81791;
DT 01-NOV-1996 (TrEMBLrel. 01, Created);
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update);
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update);
DE Polyprotein (Fragment);
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DK13;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
```

RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."
 RL Procl. Natl. Acad. Sci. U.S.A. 99:4942-4946(1992)
 DR EMBL; M84832; AAA45698.1; -
 DE InterPro; IPR002522; HCV_capsid.
 DR Pfam; PF01543; HCV_capsid; 1.
 FI: NCBI TER 13
 SC SEQUENCE 13 AA, 1572 MW, 464F97E1A42FC7A3 CRC64;

Query Match 27.9%; Score 29; DB 12; Length 13;
 Best local similarity 45.5%; Pred. No. 7.5e+02;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 SNETPKYKYP 13
 DB 3 TNPKPQKTKR 13

RESULT 11

Q81772 PRELIMINARY; PRT; 13 AA.
 AC Q81772;
 DT 01-NOV-1996 (TRENBLREL 01, Created)
 DT 01-NOV-1996 (TRENBLREL 01, Last sequence update)
 DT 01-DEC-2001 (TRENBLREL 19, Last annotation update)
 DE Polypeptide (Fragment).
 GN POLYPROTEIN.
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive strand viruses, no RNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID 11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S9;
 RX MEDLINE 92279243; PubMed 1317579;
 RA Bukh J., Purcell R.H., Miller R.H.;
 RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."
 RL Procl. Natl. Acad. Sci. U.S.A. 99:4942-4946(1992)
 DR EMBL; M84833; AAA45690.1; -
 DE InterPro; IPR002522; HCV_capsid.
 DR Pfam; PF01543; HCV_capsid; 1.
 FI: NCBI TER 13
 SC SEQUENCE 13 AA, 1572 MW, 464F97E1A42FC7A3 CRC64;

Query Match 27.9%; Score 29; DB 12; Length 13;
 Best local similarity 45.5%; Pred. No. 7.5e+02;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 SNETPKYKYP 13
 DB 3 TNPKPQKTKR 13

RESULT 12

Q81763 PRELIMINARY; PRT; 13 AA.
 AC Q81763;
 DT 01-NOV-1996 (TRENBLREL 01, Created)
 DT 01-NOV-1996 (TRENBLREL 01, Last sequence update)
 DT 01-DEC-2001 (TRENBLREL 19, Last annotation update)
 DE Polypeptide (Fragment).
 GN POLYPROTEIN.
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive strand viruses, no RNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID 11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S9;
 RX MEDLINE 92279243; PubMed 1317579;
 RA Bukh J., Purcell R.H., Miller R.H.;
 RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."
 RL Procl. Natl. Acad. Sci. U.S.A. 99:4942-4946(1992)
 DR EMBL; M84836; AAA45697.1; -

RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."
 RL Procl. Natl. Acad. Sci. U.S.A. 99:4942-4946(1992)
 DR EMBL; M84832; AAA45698.1; -
 DE InterPro; IPR002522; HCV_capsid.
 DR Pfam; PF01543; HCV_capsid; 1.
 FI: NCBI TER 13
 SC SEQUENCE 13 AA, 1572 MW, 464F97E1A42FC7A3 CRC64;

Query Match 27.9%; Score 29; DB 12; Length 13;
 Best local similarity 45.5%; Pred. No. 7.5e+02;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 SNETPKYKYP 13
 DB 3 TNPKPQKTKR 13

RESULT 13

Q81773 PRELIMINARY; PRT; 13 AA.
 AC Q81773;
 DT 01-NOV-1996 (TRENBLREL 01, Created)
 DT 01-NOV-1996 (TRENBLREL 01, Last sequence update)
 DT 01-DEC-2001 (TRENBLREL 19, Last annotation update)
 DE Polypeptide (Fragment).
 GN POLYPROTEIN.
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive strand viruses, no RNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID 11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S9;
 RX MEDLINE 92279243; PubMed 1317579;
 RA Bukh J., Purcell R.H., Miller R.H.;
 RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."
 RL Procl. Natl. Acad. Sci. U.S.A. 99:4942-4946(1992)
 DR EMBL; M84838; AAA45691.1; -
 DE InterPro; IPR002522; HCV_capsid.
 DR Pfam; PF01543; HCV_capsid; 1.
 FI: NCBI TER 13
 SC SEQUENCE 13 AA, 1572 MW, 464F97E1A42FC7A3 CRC64;

Query Match 27.9%; Score 29; DB 12; Length 13;
 Best local similarity 45.5%; Pred. No. 7.5e+02;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 SNETPKYKYP 13
 DB 3 TNPKPQKTKR 13

RESULT 14

Q81763 PRELIMINARY; PRT; 13 AA.
 AC Q81763;
 DT 01-NOV-1996 (TRENBLREL 01, Created)
 DT 01-NOV-1996 (TRENBLREL 01, Last sequence update)
 DT 01-DEC-2001 (TRENBLREL 19, Last annotation update)
 DE Polypeptide (Fragment).
 GN POLYPROTEIN.
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive strand viruses, no RNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID 11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S9;
 RX MEDLINE 92279243; PubMed 1317579;
 RA Bukh J., Purcell R.H., Miller R.H.;
 RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."
 RL Procl. Natl. Acad. Sci. U.S.A. 99:4942-4946(1992)
 DR EMBL; M84839; AAA45691.1; -
 DE InterPro; IPR002522; HCV_capsid.
 DR Pfam; PF01543; HCV_capsid; 1.
 FI: NCBI TER 13

W: 4649761A42F774...E V4;
S: Score 29; DP 12; Length 13;
A: Pred. No. 7; Labels 0; Gaps 0;

RT: 13 AA.
1: Created.
2: Last sequence update.
3: Last annotation update.

Flaviviridae, H 10A 0100: Flaviviridae;

1100679;
Virus P.H.;
Gen. acc. according to: H 10A 0100: Flaviviridae;
H 10A 0100: Flaviviridae;
H 10A 0100: Flaviviridae;
H 10A 0100: Flaviviridae;

W: 4649761A42F774...E V4;
S: Score 29; DP 12; Length 13;
A: Pred. No. 7; Labels 0; Gaps 0;

2003, 07:00:26

XX
PS Claim 11; Page 79, 79pp, English.
XX
CC The present peptide sequence represents a specifically tailored membrane
CC binding element. The invention relates to a suitable derivative (A) of a
CC suitable polypeptide (B), which comprises at least 1 heptapeptide
CC membrane binding element (MBE) of low membrane affinity. Equivalently
CC associated with (1) MBE interact, independently and with thermodynamic
CC activity, with components of cellular or artificial membranes exposed
CC to extracellular fluids. (A) are used to treat disorders treatable with
CC (1) itself, specifically inflammation or any other complement-related
CC disorder such as rheumatoid arthritis, graft rejection, myocardial
CC infarction, sepsis, rheumatoid arthritis and many others; including
CC application to immobilizing devices and therapeutic devices that also
CC treat allergy, induce weight loss, or treat asthma; (A) are also used
CC as immune modulators for treating multiple sclerosis. (A) are administered
CC orally, typically, by injection or inhalation at 0.01 to 10 (preferably
CC 0.1 to 10) mg/kg/day.
XX
XX
XX

XX Sequence 20 AA;

Query Match 100.0%, Score 104, BB 19, Length 20;

Best Local Similarity 100.0%; Pred No 1 to 08;

Matches 20; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPSTHTFFFFFFPPKWSG 20

Db 1 SPSTHTFFFFFFPPKWSG 20

RESULT 2

AAV59857

ID AAV59857 standard; peptide, 20 AA.

XX AAV59857;

XX AAV59857;

XX 08-MAY-2000 (first entry)

XX Membrane binding element used in anti-angiogenic polypeptide

XX Anti-angiogenic, angiogenesis inhibitor, membrane binding element;

XX cancer, tumor, therapy.

XX Synthetic.

XX W020000404 A1

XX 27-JAN-2000.

XX 16-JUL-1999; 94WO-GB04282.

XX 16-JUL-1999; 94GB 001505.

XX (ADPR-) ADPROTECH PLC.

XX Smith PAC, Raleigh NC, Stewart M, Clark VF,

XX WPI; 2000-04-06/16.

XX

XX New soluble inhibition of anti-angiogenic polypeptide useful for

XX treatment of primary or secondary cancer, which is advantageously attached

XX membrane-binding elements for targeting

XX

XX Claim 12; Page 82, 82pp, English.

XX

XX The present polypeptide is a claimed derivative of a lysine-rich peptide

XX membrane binding element (MBE) that can be utilised in novel

XX membrane derivatives (D) of anti-angiogenic polypeptides (B) for

XX treatment of cancer, which comprises at least one heptapeptide

XX membrane affinity that are advantageously attached to a soluble

XX anti-angiogenic polypeptide such as a non-catalytic region of human

XX plasminogen fragments of related proteins containing heptapeptide

XX heptapeptide fragments of collagen or fibrin, neutralising

XX anti-platelet binding receptors for angiogenic mediators, and
XX antagonists of integrins involved in angiogenesis. The MBEs
XX interact specifically with thermodynamic activity, with
XX components of the vascular endothelium. (A) provide targeted
XX delivery of the anti-angiogenic polypeptide to the vascular endothelium,
XX sites of active angiogenesis, particularly the vascular endothelium,
XX and therefore increase the local concentration and reduce the risk
XX of adverse effects on normal tissues elsewhere in the vasculature.
XX They are used in a claimed method of treatment of primary or
XX secondary tumour.

XX Sequence 20 AA;

Query Match 100.0%, Score 104, BB 21, Length 20;

Best Local Similarity 100.0%; Pred No 1 to 08;

Matches 20; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPSTHTFFFFFFPPKWSG 20

Db 1 SPSTHTFFFFFFPPKWSG 20

RESULT 3

AAV59857

ID ABB81239 standard; peptide, 20 AA.

XX ABB81239;

XX ABB81239;

XX 20 AUG-2002 (first entry)

XX Antibacterial membrane binding peptide SEQ ID NO:6.

XX Antibacterial, glycopeptide, lipopeptide, and other elements

XX bacterial infection, vancomycin, lipopeptide, lipopeptide

XX antibiotic.

XX Synthetic.

XX W020000404 A1.

XX 10-MAY-2002.

XX 02 NOV 2001; 2001WO-GB04867.

XX 04 NOV 2001; 2000JP-0004904.

XX (UNCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX (ADPR-) ADPROTECH LTD.

XX Cooper MA, Parley JR;

XX WPI; 2002-04-04/50.

XX

XX Antibacterial compound, useful for the treatment of a bacterial

XX infection by high gram positive or negative bacteria, comprises a

XX conjugate of glycopeptide and peptide membrane association element

XX

XX Claim 3, Page 37, 64pp, English.

XX

XX The present invention relates to an anti-bacterial compound comprising
XX a conjugate of glycopeptide and peptide membrane-association element.
XX (1) comprises the formula V (W, X), where V is a glycopeptide moiety that
XX inhibits peptidoglycan biosynthesis in bacteria, W is a linking group;
XX W is a peptide membrane-association element, and X is H or a membrane-
XX insertive element. Also described: (1) a method of treating or preventing
XX a bacterial infection, comprising the administration of (1); and (2) use
XX of (1) in the manufacture of a medicament for the treatment or prevention
XX of a bacterial infection. (1) are used in the manufacture of a medicament
XX for the treatment of glycolysis of a bacterial infection in a human or
XX animal body, including both the gram positive and gram negative bacteria
XX including *Staphylococcus* sp., *Escherichia* sp., *Pseudomonas* sp.,
XX *Streptococcus* sp., *Vibrio* sp., *Neisseria* sp., *Haemophilus* sp.,
XX *Legionella* sp., *Mycobacterium* sp., *Acetivibrio* sp.,

Amplified, particularly antibiotic resistant
are also useful as wound treatment agents to
treat matrix proteins, especially fibronectin,
and for prophylactic use in dental treatment as
in conjunction with antibiotic prophylaxis. (1)
Bacterial membranes which have a higher
sphingolipids than the eukaryotic organisms, also
ion of membrane associated biosynthetic proteins.
served antimicrobial activity of an antiviral
to treat the antibiotic resistant bacterial
which represent peptides given in the
cancer invention.

Query Match 44.3% Score 46 DP 13 Length 14
Best Local Similarity 100.0% Pred. No. 718605
Matches 9; Conservative 0; Mismatches 0; Gaps 0;

QY 9 KKKYFSPK 17
DP 1 KKKYFSPK 9
|||||
|||||

RESULT 5
AAB50062
ID AAB50062 standard; Peptide: 18 AA.
XX AC AAB50062;
XX DT 19-MAR-2001 (first entry)
XX DE Protein kinase C substrate H1.
XX KW MLCK; MCK; autoimmune disorder; Large NIK Related Kinase 1;
XX PW wound healing; Fertilization disease; inflammatory disease; tumor;
XX KW infection; allergy; MCK1.
XX OS Unidentified.
XX PN WO200073458-A1.
XX PD 07-DEC-2000.
XX PF 26-MAY-2000; 250060-US14896.
XX PR 28-MAY-1999; 99LS-0126781.
XX PA (IMMV) IMMUNEX CCRP.
XX PI Bird TA, Virca GE, Martin U, Andersen DM;
XX DR WPI; 2001-061546/C7.
XX PT Novel murine and human kinase nucleic acids useful for treating
XX PT inflammations, infections, tumors, allergies, autoimmune diseases, and
XX PT for stimulating or suppressing immune responses
XX PS Example 5; Page 69; 106pp; English.

The present invention relates to kinases MCK1, MCK2, MCK3 and MCK4
and -2; see AAB50062-50067, and MCK1; see AAB50062. The kinases of
the present invention are useful for treating a variety of disorders
listed in the disclosure of the specification, including autoimmune
disorders, allergic reactions, wound or lymphoid cell deficiencies,
wound healing and tissue repair and regenerative, tumor, leukemia and
ulcers, periodontal disease, inflammatory diseases, tumors and
bacterial, viral or fungal infection. The present invention is a peptide
kinase substrate used in the present invention to investigate the
substrate specificity of MLCK-1.

Query Match 43.3% Score 45 DP 12 Length 14
Best Local Similarity 100.0% Pred. No. 517
Matches 9; Conservative 0; Mismatches 0; Gaps 0;

QY 11 KKKYFSPK 19
DP 1 KKKYFSPK 9
|||||
|||||

CC phosphorylated state indicates the presence of PK activity. The method
CC and products can be used in direct selection. They can be used for
CC screening for compounds which affect cellular events, including
CC receptor-ligand binding, protein-protein interactions, kinase
CC activation, which signal to the target kinase.
XX
SQ Sequence 9 AA;

Query Match 44.3% Score 46 DP 13 Length 14
Best Local Similarity 100.0% Pred. No. 718605
Matches 9; Conservative 0; Mismatches 0; Gaps 0;

QY 9 KKKYFSPK 17
DP 1 KKKYFSPK 9
|||||
|||||

RESULT 5
AAB50062
ID AAB50062 standard; Peptide: 18 AA.
XX AC AAB50062;
XX DT 19-MAR-2001 (first entry)
XX DE Protein kinase C substrate H1.
XX KW MLCK; MCK; autoimmune disorder; Large NIK Related Kinase 1;
XX PW wound healing; Fertilization disease; inflammatory disease; tumor;
XX KW infection; allergy; MCK1.
XX OS Unidentified.
XX PN WO200073458-A1.
XX PD 07-DEC-2000.
XX PF 26-MAY-2000; 250060-US14896.
XX PR 28-MAY-1999; 99LS-0126781.
XX PA (IMMV) IMMUNEX CCRP.
XX PI Bird TA, Virca GE, Martin U, Andersen DM;
XX DR WPI; 2001-061546/C7.
XX PT Novel murine and human kinase nucleic acids useful for treating
XX PT inflammations, infections, tumors, allergies, autoimmune diseases, and
XX PT for stimulating or suppressing immune responses
XX PS Example 5; Page 69; 106pp; English.

The present invention relates to kinases MCK1, MCK2, MCK3 and MCK4
and -2; see AAB50062-50067, and MCK1; see AAB50062. The kinases of
the present invention are useful for treating a variety of disorders
listed in the disclosure of the specification, including autoimmune
disorders, allergic reactions, wound or lymphoid cell deficiencies,
wound healing and tissue repair and regenerative, tumor, leukemia and
ulcers, periodontal disease, inflammatory diseases, tumors and
bacterial, viral or fungal infection. The present invention is a peptide
kinase substrate used in the present invention to investigate the
substrate specificity of MLCK-1.

Query Match 43.3% Score 45 DP 12 Length 14
Best Local Similarity 100.0% Pred. No. 517
Matches 9; Conservative 0; Mismatches 0; Gaps 0;

QY 11 KKKYFSPK 19
DP 1 KKKYFSPK 9
|||||
|||||

CC phosphorylated state indicates the presence of PK activity. The method
CC and products can be used in direct selection. They can be used for
CC screening for compounds which affect cellular events, including
CC receptor-ligand binding, protein-protein interactions, kinase
CC activation, which signal to the target kinase.
XX
SQ Sequence 9 AA;

Query Match 44.3% Score 46 DP 13 Length 14
Best Local Similarity 100.0% Pred. No. 718605
Matches 9; Conservative 0; Mismatches 0; Gaps 0;

QY 9 KKKYFSPK 17
DP 1 KKKYFSPK 9
|||||
|||||

RESULT 5
AAB50062
ID AAB50062 standard; Peptide: 18 AA.
XX AC AAB50062;
XX DT 19-MAR-2001 (first entry)
XX DE Protein kinase C substrate H1.
XX KW MLCK; MCK; autoimmune disorder; Large NIK Related Kinase 1;
XX PW wound healing; Fertilization disease; inflammatory disease; tumor;
XX KW infection; allergy; MCK1.
XX OS Unidentified.
XX PN WO200073458-A1.
XX PD 07-DEC-2000.
XX PF 26-MAY-2000; 250060-US14896.
XX PR 28-MAY-1999; 99LS-0126781.
XX PA (IMMV) IMMUNEX CCRP.
XX PI Bird TA, Virca GE, Martin U, Andersen DM;
XX DR WPI; 2001-061546/C7.
XX PT Novel murine and human kinase nucleic acids useful for treating
XX PT inflammations, infections, tumors, allergies, autoimmune diseases, and
XX PT for stimulating or suppressing immune responses
XX PS Example 5; Page 69; 106pp; English.

The present invention relates to kinases MCK1, MCK2, MCK3 and MCK4
and -2; see AAB50062-50067, and MCK1; see AAB50062. The kinases of
the present invention are useful for treating a variety of disorders
listed in the disclosure of the specification, including autoimmune
disorders, allergic reactions, wound or lymphoid cell deficiencies,
wound healing and tissue repair and regenerative, tumor, leukemia and
ulcers, periodontal disease, inflammatory diseases, tumors and
bacterial, viral or fungal infection. The present invention is a peptide
kinase substrate used in the present invention to investigate the
substrate specificity of MLCK-1.

Query Match 43.3% Score 45 DP 12 Length 14
Best Local Similarity 100.0% Pred. No. 517
Matches 9; Conservative 0; Mismatches 0; Gaps 0;

QY 11 KKKYFSPK 19
DP 1 KKKYFSPK 9
|||||
|||||

RESULT 6

AAR71783

ID AAR71783 standard; peptide; 10 AA

XX

AC AAR71783;

DT 01-OCT-1995 (first entry)

DE Peptide neutralising toxicity of Lipid A.

XX Endotoxin; Lipid A; septic shock; lipopolysaccharide.

XX Synthetic

OS

XX WO9638163-A1.

XX

XX PD 02-FEB-1995.

XX

XX 21-JUL-1994; 94WO-EP02413.

XX

XX 26-JUL-1993; same as 94WO-EP02413.

XX

XX (BIOS-) BIOSYNTH SRL.

XX

XX Porro M;

XX

XX WPI; 1995-073100/10.

XX

XX New peptide(s) for neutralising LPS endotoxin - comprising
PT repeating units of a basic amino acid or basic and hydrophobic
PT amino acids

XX

XX Claim 14, Page 21, 26pp, English.

XX

XX New peptides are claimed which are linear or cyclic peptides which
CC include units of formula (A)n, where A is the cationic amino acid lys
CC et Arg and n is 7 to 10. (A)n/m, where A is Lys or Arg, B is the hydrophobic
CC amino acid Val, Leu, Ile, Tyr, Phe or Trp, and m is 3 or greater; and
CC (ABC)p, where A is Lys or Arg, B and C are Val, Leu, Ile, Tyr, Phe or
CC Trp, and p is 2 or greater.XX The peptides bind to Lipid A of endotoxins and do not exhibit haemolytic
CC activity. Hence they can be used therapeutically to treat septic shock
CC and also in vitro to detoxify vaccines, drug solutions, injectable
CC nutrient solutions, etc.XX The present sequence is a specifically claimed example of the new
CC peptides.

XX

SQ Sequence 10 AA;

XX

Query Match 42.3%; Score 44; DB 16; Length 10;

Res. 1; 100% Similarity; 80.0%, Pred. No. 4.4;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

XX

CY 9 KKKKKKKKKK 17

|||||

Cb 1 KKKKKKKKKK 10

XX

RESULT 7

AAW21600

ID AAW21600 standard; peptide; 10 AA.

XX

AC AAW21600;

XX

DT 26-AUG-1997 (first entry)

XX

DE Antibiotic potentiating peptide #10.

XX

XX Potentiates antibiotic; microbial infection; lipopolysaccharide.

XX

XX Potentiates antibiotic; microbial infection; lipopolysaccharide.

XX

XX Potentiates antibiotic; microbial infection; lipopolysaccharide.

XX

OS Synthetic

XX WO9638163-A1.

XX

XX PD 05-DEC-1996.

XX

XX 29-MAY-1996; 94WO-EP02313.

XX

XX 31-MAY 1995; 95US-0455112.

XX

XX (BIOS-) BIOSYNTH SRL.

XX

XX Porro M; Varra M;

XX

XX WPI; 1997-034005/03.

XX

XX Potentiating activity of antibiotic with peptide containing cationic

XX amino acid sequence - reduces dose of antibiotic required

XX

XX Claim 16; Page 25; 37pp; English.

XX

XX The sequences given in AAW21600 (10) represent peptides which act to

XX potentiates the activity of an antibiotic when they are combined with

XX with the antibiotic. Compositions containing these peptides are used

XX to treat or prevent microbial infections. These peptides bind to

XX lipopolysaccharide on the surface of bacteria and may increase permeability of

XX the outer bacterial membrane to the antibiotic, allowing a reduction

XX in the dose of antibiotic required by 10-100% of the normal dose for

XX in vivo or in vitro application. Any toxic side effects are

XX correspondingly reduced.

XX

XX Sequence 10 AA;

XX

XX Query Match 42.3%; Score 44; DB 16; Length 10;

XX Res. 1; 100% Similarity; 80.0%, Pred. No. 4.4;

XX Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

XX

CY 9 KKKKKKKKKK 17

|||||

Cb 1 KKKKKKKKKK 10

XX

XX RESULT 8

XX AAW56912

XX ID AAW56912 standard; peptide; 10 AA.

XX

XX AC AAW56912;

XX

XX DT 14-APR-2000 (first entry)

XX

XX DE Peptide contained in a vaccine for bacterial infection.

XX

XX Vaccine, gram-negative infection, oral + i.v., i.p., parenteral infection;

XX sepsis; septic shock; toxemia; cyclic.

XX

XX OS Synthetic.

XX

XX EP976402-A2.

XX

XX PD 02-FEB-2000.

XX

XX PF 27-JUL-1969; 99EP-0202476.

XX

XX PR 29-JUL-1968; 98US-0124280.

XX

XX PA (BIOS-) BIOSYNTH SRL.

XX

XX PI Porro M;

XX

XX WPI; 2000 129104/12.

XX

XX New vaccine for prevention of gram-negative bacterial infections and

XX endotoxin related disorders, comprising complex of peptide and LPS

XX

KW Human; catalyst; diacylglycerol; DAG; phosphatidic acid; DAG modulator;
 KW diacylglycerol kinase zeta, DGG, MAFK; domain;
 KW myristoylated alanine rich C-kinase substrate.

XX Homo sapiens.

XX US6221658-B1.

XX 24 APR-2001.

XX 25-AUG-1999; 99US-0382911.

XX 22 APR-1999; 98US-0016210.

XX 22-APR-1997; 97US-0841483.

XX (UTAH) UNIV UTAH RES FOUND.

XX Prescott SM, Runtang M, Tang W, Topham M;

XX WFI; 3001 327248/34.

XX New DNAs of the human diacylglycerol kinase, useful for modulating the
 PT levels of diacylglycerol kinase in cells to catalyze the conversion of
 PT diacylglycerol to phosphatidic acid, therefore increasing phosphatidic
 PT acid levels.

PS Example 12; Column 26; 74pp; English.

XX The patent discloses novel human diacylglycerol kinase (DAGK) isoforms
 CC namely diacylglycerol kinase epsilon, diacylglycerol kinase zeta,
 CC diacylglycerol kinase eta and their corresponding cDNAs. Human
 CC diacylglycerol kinase cDNA is useful for coding human diacylglycerol
 CC kinase, which is useful for catalyzing the conversion of diacylglycerol
 CC to phosphatidic acid. In particular, the human diacylglycerol kinase
 CC and its DNA are useful for decreasing intracellular levels of diacyl-
 CC glycerol (DAG) and for increasing intracellular levels of phosphatidic
 CC acid in cells.

CC The present sequence is the myristoylated alanine-rich C-kinase
 CC substrate (MAKRS) domain of human diacylglycerol kinase (DAGK)
 CC zeta protein.

XX SO Sequence 18 AA;

Query Match 39.5%; Score 40; DB 22; Length 18;

Best Local Similarity 80.0%; Pred. No. 31;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 9 KKKKPSFKK 18

|||||

Db 4 KKKKPSFKK 13

Search completed: March 3, 2003, 06:56:01
 Job time : 34 secs


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? MOLECULE TYPE: Peptide
? SEQUENCE DESCRIPTION: SEQ ID NO: 3
US-09-884-681-8

Query Match: 44.23, Score 46, DE 10, Length 10,
Best Local Similarity 90.03, Field No 23,
Matches 9, Conservative 0, Mismatches 0, Indels 0, Gaps 0

CY 3 XXXXXXXX 17
DE 1 XXXXXXXX 9

RESULT 2
US-09-124-280A-12
? Sequence 42, Application NO: 09/00104280A
? Patent No. US2002034520A1
? GENERAL INFORMATION:
? APPLICANT: FORTO, Massimo
? TITLE OF INVENTION: VACCINES FOR PREVENTION OF GRAM-
? TITLE OF INVENTION: REMANINE BACTERIAL INFECTIONS AND ENDOGEN RELATES ILLIATED
? NUMBER OF SEQUENCES: 45
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Hedman, Gibson & Costigan
? STREET: 1185 Avenue of the Americas
? CITY: New York
? STATE: New York
? COUNTRY: USA
? ZIP: 10036
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
? COMPUTER: IBM PS/2
? OPERATING SYSTEM: DOS
? SOFTWARE: Word Perfect 5.1
? CURRENT APPLICATION DATA: 09/00/124-280A
? APPLICATION NUMBER: 09/00/124-280A
? FILING DATE: July 29, 1998
? CLASSIFICATION: 424
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Costigan, James V.
? REGISTRATION NUMBER: 25,669
? REFERENCE/DOCKET NUMBER: 576 008
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 302 8299
? TELEFAX: (212) 302 8299
? INFORMATION FOR SEQ ID NO: 12:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 10 amino acids
? TYPE: amino acid
? TOPOLOGY: circular
US-09-124-280A-12

Query Match: 42.33, Score 48, DE 10, Length 10,
Best Local Similarity 90.03, Field No 23,
Matches 8, Conservative 1, Mismatches 1, Indels 0, Gaps 0

CY 8 XXXXXXXX 17
DE 1 XXXXXXXX 10

RESULT 3
US-09-124-280A-12
? Sequence 42, Application NO: 09/00104280A
? Patent No. US2002034520A1
? GENERAL INFORMATION:
? APPLICANT: FORTO, Massimo
? TITLE OF INVENTION: VACCINES FOR PREVENTION OF GRAM-
? TITLE OF INVENTION: REMANINE BACTERIAL INFECTIONS AND ENDOGEN RELATES ILLIATED
? NUMBER OF SEQUENCES: 45
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Hedman, Gibson & Costigan
? STREET: 1185 Avenue of the Americas
? CITY: New York
? STATE: New York
? COUNTRY: USA
? ZIP: 10036
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
? COMPUTER: IBM PS/2
? OPERATING SYSTEM: DOS
? SOFTWARE: Word Perfect 5.1
? CURRENT APPLICATION DATA: 09/00/124-280A
? APPLICATION NUMBER: 09/00/124-280A
? FILING DATE: July 29, 1998
? CLASSIFICATION: 424
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Costigan, James V.
? REGISTRATION NUMBER: 25,669
? REFERENCE/DOCKET NUMBER: 576 008
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 302 8299
? TELEFAX: (212) 302 8299
? INFORMATION FOR SEQ ID NO: 12:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 10 amino acids
? TYPE: amino acid
? TOPOLOGY: circular
US-09-124-280A-12
```

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? FILE REFERENCE: 012960
? CURRENT APPLICATION NUMBER: 09/00104280A
? CURRENT FILING DATE: 2001-10-24
? PRIOR APPLICATION NUMBER: US 09/101,751
? PRIOR FILING DATE: 1999-01-29
? PRIOR APPLICATION NUMBER: WO 97/13113
? PRIOR FILING DATE: 1996-11-27
? PRIOR APPLICATION NUMBER: US 08/766,846
? PRIOR FILING DATE: 1996-09-21
? PRIOR APPLICATION NUMBER: US 08/701,124
? PRIOR FILING DATE: 1996-08-21
? PRIOR APPLICATION NUMBER: US 08/563,368
? PRIOR FILING DATE: 1996-11-28
? NUMBER OF SEQ ID NOS: 94
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 16
? LENGTH: 19
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Synthetic
US-09-884-681-8

Query Match: 37.83, Score 39, DE 9, Length 19,
Best Local Similarity 90.03, Field No 23,
Matches 9, Conservative 4, Mismatches 4, Indels 0, Gaps 0

CY 4 XXXXXXXX 19
DE 1 XXXXXXXX 16

RESULT 4
US-09-124-280A-42
? Sequence 42, Application NO: 09/00104280A
? Patent No. US2002034520A1
? GENERAL INFORMATION:
? APPLICANT: FORTO, Massimo
? TITLE OF INVENTION: VACCINES FOR PREVENTION OF GRAM-
? TITLE OF INVENTION: REMANINE BACTERIAL INFECTIONS AND ENDOGEN RELATES ILLIATED
? NUMBER OF SEQUENCES: 45
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Hedman, Gibson & Costigan
? STREET: 1185 Avenue of the Americas
? CITY: New York
? STATE: New York
? COUNTRY: USA
? ZIP: 10036
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
? COMPUTER: IBM PS/2
? OPERATING SYSTEM: DOS
? SOFTWARE: Word Perfect 5.1
? CURRENT APPLICATION DATA: 09/00/124-280A
? APPLICATION NUMBER: 09/00/124-280A
? FILING DATE: July 29, 1998
? CLASSIFICATION: 424
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Costigan, James V.
? REGISTRATION NUMBER: 25,669
? REFERENCE/DOCKET NUMBER: 576 008
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 302 8299
? TELEFAX: (212) 302 8299
? INFORMATION FOR SEQ ID NO: 42:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 10 amino acids
? TYPE: amino acid
? TOPOLOGY: circular
US-09-124-280A-42
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Query Match 35.64; Score 37; DP 9; Length 207
Best Local Similarity 52.84; Pred. No. 45;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SPSNETPKYKYYR 13
DB 2 SVMWESPKYKYNQ 14

RESULT 7
US-09-999-724-38
Sequence 38, Application US/09999724
Publication No. US20010022355A1
GENERAL INFORMATION: THOMAS J.
APPLICANT: WICKHAM, IMRE
APPLICANT: KOVESDI, IMRE
TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER
FILE REFERENCE: 212960
CURRENT APPLICATION NUMBER: US/09/999,724
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: US 09/101,751
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: WO 98US19150
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 08/701,816
PRIOR FILING DATE: 1996-08-31
PRIOR APPLICATION NUMBER: US 08/701,124
PRIOR FILING DATE: 1996-08-21
PRIOR APPLICATION NUMBER: US 08/563,368
PRIOR FILING DATE: 1995-11-28
NUMBER OF SEQ ID NOS: 94
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 38
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-999-724-38

Query Match 33.78; Score 35; DP 9; Length 15;
Best Local Similarity 60.04; Pred. No. 43;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 NETPKYKYYR 13
DB 1 NDTPKYKYYR 10

RESULT 8
US-09-954-866-30
Sequence 30, Application US/09864866
Patent No. US2002012656A1
GENERAL INFORMATION:
APPLICANT: Lloyd, R. Stephen
APPLICANT: McCulloch, Amanda K.
APPLICANT: Nguyen, Khoa
TITLE OF INVENTION: DNA REPAIR POLYMERASES AND METHODS OF USE
FILE REFERENCE: 265,001,701
CURRENT APPLICATION NUMBER: US/03/864,866
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/266,279
PRIOR FILING DATE: 2000-05-23
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn version 3.0
SEQ ID NO 30
LENGTH: 8
TYPE: PRT

Query Match 35.64; Score 37; DP 9; Length 207
Best Local Similarity 52.84; Pred. No. 45;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SPSNETPKYKYYR 13
DB 2 SVMWESPKYKYNQ 14

RESULT 7
US-09-999-724-38
Sequence 38, Application US/09999724
Publication No. US20010022355A1
GENERAL INFORMATION: THOMAS J.
APPLICANT: WICKHAM, IMRE
APPLICANT: KOVESDI, IMRE
TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER
FILE REFERENCE: 212960
CURRENT APPLICATION NUMBER: US/09/999,724
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: US 09/101,751
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: WO 98US19150
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 08/701,816
PRIOR FILING DATE: 1996-08-31
PRIOR APPLICATION NUMBER: US 08/701,124
PRIOR FILING DATE: 1996-08-21
PRIOR APPLICATION NUMBER: US 08/563,368
PRIOR FILING DATE: 1995-11-28
NUMBER OF SEQ ID NOS: 94
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 38
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-999-724-38

Query Match 33.78; Score 35; DP 9; Length 15;
Best Local Similarity 60.04; Pred. No. 43;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 NETPKYKYYR 13
DB 1 NDTPKYKYYR 10

RESULT 8
US-09-954-866-30
Sequence 30, Application US/09864866
Patent No. US2002012656A1
GENERAL INFORMATION:
APPLICANT: Lloyd, R. Stephen
APPLICANT: McCulloch, Amanda K.
APPLICANT: Nguyen, Khoa
TITLE OF INVENTION: DNA REPAIR POLYMERASES AND METHODS OF USE
FILE REFERENCE: 265,001,701
CURRENT APPLICATION NUMBER: US/03/864,866
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/266,279
PRIOR FILING DATE: 2000-05-23
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn version 3.0
SEQ ID NO 30
LENGTH: 8
TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: A consensus nucleic acid localization sequence
US-09-864-866-30

Query Match 32.7% Score 34; DB 10; Length 8;
Best Local Similarity 85.7% Pred No. 1.5e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 PKKKKK 13
DB 1 PKKKKK 7

RESULT 9
US-08-910-386A-53
Sequence 53, Application US/20010386A
Patent No. US2002002041A1
GENERAL INFORMATION:
APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo Liang
APPLICANT: Gong, Wen Yuan
APPLICANT: Hulbert, Scott
APPLICANT: Richter, Todd
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910-386A
FILING DATE: 13 AUG 1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 127, 132, 133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-6200
TELEFAX: (415) 576-6200

INFORMATION FOR SEQ ID NO. 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified site
LOCATION: 13
OTHER INFORMATION: Product "OTHER"
OTHER INFORMATION: /roles "Mod - 110, Mod, Thr, Asn, Lys,
OTHER INFORMATION: Ser at 61"

FEATURE:
NAME/KEY: Modified site
LOCATION: 14
OTHER INFORMATION: Product "OTHER"
OTHER INFORMATION: /roles "Mod - 110, Mod, Thr, Asn, Lys,
OTHER INFORMATION: Ser at 61"

US-08-910-386A-53
Query Match 32.7% Score 34; DB 8; Length 14;
Best Local Similarity 85.7% Pred No. 1.5e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 PKKKKK 13
DB 2 PKKKKK 8

RESULT 10
US-09-214-913-39
Sequence 87, Application US/20010187A1
Patent No. US2002018748A1
GENERAL INFORMATION:
APPLICANT: BERLIN, VIVIAN
APPLICANT: DAMAGNEZ, VERONIQUE
APPLICANT: SMITH, SUSAN E.

TITLE OF INVENTION: ASSAYS AND FRAGMENTS FOR IDENTIFYING ANTI-EPIDEM AGENTS,
TITLE OF INVENTION: AND USES RELATED THERETO
FILE REFERENCE: WIV 074 07
CURRENT APPLICATION NUMBER: US/09/214-913-39
CURRENT FILING DATE: 2001-08-11
PRIOR APPLICATION NUMBER: 09/041,990
PRIOR FILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: 09/771,212
PRIOR FILING DATE: 1996-12-20
PRIOR APPLICATION NUMBER: 09/731,119
PRIOR FILING DATE: 1996-04-11
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 97
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide that
OTHER INFORMATION: corresponds to the C-terminal of Phase of GTPase
OTHER INFORMATION: substrates
US-09-945-349-87

Query Match 32.7% Score 34; DB 9; Length 15;
Best Local Similarity 77.8% Pred No. 85;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 NETPKKKKK 12
DB 2 NETPKKKKK 11

RESULT 11
US-09-071-838-196
Sequence 19, Application US/200101838A1
Patent No. US200201838A1
GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Chad, Nir
APPLICANT: Miyase, Tomohiro
APPLICANT: Vadevati, Pamin
APPLICANT: Maragostan, Linda
APPLICANT: Harada, John
APPLICANT: Goldberg, Robert B.
TITLE OF INVENTION: Nucleic Acids That Control Seed and
TITLE OF INVENTION: Plant Development in Plants
NUMBER OF SEQUENCES: 324
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30

the 1990s, the number of people in the world who are under 15 years of age is expected to increase from 1.1 billion to 1.5 billion. The number of people aged 65 and over is expected to increase from 200 million to 400 million. The number of people aged 15 and over is expected to increase from 3.5 billion to 4.5 billion. The number of people aged 15 and over is expected to increase from 3.5 billion to 4.5 billion. The number of people aged 15 and over is expected to increase from 3.5 billion to 4.5 billion.

[illegible][illegible]

the 1990s, the number of people in the world who are under 15 years of age is expected to increase from 1.1 billion to 1.5 billion. The number of people aged 65 and over is expected to increase from 200 million to 400 million. The number of people aged 15 and over is expected to increase from 3.5 billion to 4.5 billion. The number of people aged 15 and over is expected to increase from 3.5 billion to 4.5 billion. The number of people aged 15 and over is expected to increase from 3.5 billion to 4.5 billion.

[illegible]

Score 33; 14
Pred. NO. 14
Mismatched

000007
000000

Author: Producing : P
Description/Translation:
P
R# 98009/983,067
C# 23
SP 034735/2001
AP 034735/2001
CP 034735/2001
PP 034735/2001
OP 034735/2001
IP 034735/2001
EP 1417/2000
TP 034735/2001
AP 034735/2001

100-443887-1000

```
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: polypeptide
US-09-950-692-4
```

```
Query Match 30.8% Score 32; DB 10; Length 10;
Best Local Similarity 75.0%; Pos. No. 1.0e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy 5 ETPPYKK 12
   :|||
Cb 2 KPEPKKK 9
```

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Search completed: March 3, 2003, 07:02:11
Job time : 13 secs
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COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Patent Release #103, Version #1.03
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09-214-913-39
 FILING DATE: 16-MAR-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/ACKER NUMBER: 60/916,210
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201 343-1684
 TELEFAX: 201 343-1684
 TELEX: 133521
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 FRAGMENT TYPE: internal
 US-09-214-913-39-12

Query Match 38.5%; Score 40; DB 2; Length 18;
 Best Local Similarity 37.5%; Pred No. 14;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 KRFSEKKS 19
 |||||
 Db 1 KRFSEKKS 8

RESULT 9

US-08-841-483-15
 Sequence 15, Application US/0841483P
 GENERAL INFORMATION:
 APPLICANT: Prescott, Steven M.
 APPLICANT: Bunting, Michaeline
 APPLICANT: Tang, Wen
 APPLICANT: Tang, Wen
 APPLICANT: Tang, Wen
 APPLICANT: Tang, Wen
 TITLE OF INVENTION: Methods of Use Thereof
 FILE REFERENCE: 60/916,210
 CURRENT APPLICATION NUMBER: US/08-841-483-15
 EARLIER FILING DATE: 1997-04-22
 EARLIER APPLICATION NUMBER: 60/916,210
 PRIOR FILING DATE: 1997-04-22
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO: 15
 LENGTH: 18
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Peptide: Synthetic
 OTHER INFORMATION: peptide
 US-08-841-483-15

Query Match 38.5%; Score 40; DB 2; Length 18;
 Best Local Similarity 37.5%; Pred No. 14;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 KRFSEKKS 12
 |||||
 Db 4 KRFSEKKS 13

RESULT 10
 US-09-382-911-15
 Sequence 15, Application US/09382911P
 GENERAL INFORMATION:
 APPLICANT: Prescott, Steven M.
 APPLICANT: Bunting, Michaeline
 APPLICANT: Tang, Wen
 APPLICANT: Tang, Wen
 APPLICANT: Tang, Wen
 APPLICANT: Tang, Wen
 TITLE OF INVENTION: Methods of Use Thereof
 FILE REFERENCE: 60/916,210
 CURRENT APPLICATION NUMBER: US/09-382-911-15
 PRIOR FILING DATE: 1997-04-22
 PRIOR APPLICATION NUMBER: 60/916,210
 PRIOR FILING DATE: 1997-04-22
 NUMBER OF SEQ ID NOS: 33
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO: 15
 LENGTH: 18
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Peptide: Synthetic
 OTHER INFORMATION: peptide
 US-09-382-911-15

Query Match 38.5%; Score 40; DB 4; Length 18;
 Best Local Similarity 37.5%; Pred No. 9.8;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 KRFSEKKS 18
 |||||
 Db 4 KRFSEKKS 13

RESULT 11

US-09-101-751A-36
 Sequence 36, Application US/09101751A
 GENERAL INFORMATION:
 APPLICANT: WICKHAM, THOMAS J.
 APPLICANT: WICKHAM, THOMAS J.
 APPLICANT: WICKHAM, THOMAS J.
 APPLICANT: WICKHAM, THOMAS J.
 APPLICANT: WICKHAM, THOMAS J.
 APPLICANT: WICKHAM, THOMAS J.
 TITLE OF INVENTION: Methods of Use Thereof
 FILE REFERENCE: 60/916,210
 CURRENT APPLICATION NUMBER: US/09-101-751A
 PRIOR FILING DATE: 1997-04-22
 PRIOR APPLICATION NUMBER: 60/916,210
 PRIOR FILING DATE: 1997-04-22
 NUMBER OF SEQ ID NOS: 94
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO: 36
 LENGTH: 19
 TYPE: PRT
 ORGANISM: Unknown Organism
 FEATURE:
 NAME/REF: misc feature
 LOCATION: (1..1)
 OTHER INFORMATION: Description of Unknown Organism: Artificial
 OTHER INFORMATION: Sequence
 US-09-101-751A-36

Query Match 37.5%; Score 39; DB 4; Length 19;
 Best Local Similarity 50.0%; Pred. No. 14;

||||:|||||
Db 3 PPKKKKKPPPP 15

RESULT 15

US-08-456-112B-42
Sequence 42, Application US/08456112P
Patent No. 5834430
GENERAL INFORMATION:
APPLICANT: POTO, Massimo
TITLE OF INVENTION: POTENTIATION OF ANTIBIOTICS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hedman, Gibson & Costigan
STREET: 1285 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Disette, 3.50 inch, 1.44 Mb storage
COMPUTER: IFAHNG PCP 486
OPERATING SYSTEM: DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456-112B
FILING DATE: May 31, 1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Costigan, James V.
REGISTRATION NUMBER: 25,669
REFERENCE/DOCKET NUMBER: 576-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 302-8989
TELEFAX: (212) 302-8998
INFORMATION FOR SEQ ID NO. 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: circular
US-08-456-112B-42

Query Match 35.63; Score 37; DB 2; Length 10;
Best Local Similarity 70.93, Prod No. 15;
Matches 7; Complement 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 PPKKKKKPP 16
||||:|
Db 1 PPKKKKKPP 9

Search completed: March 3, 2003, 07:00:47
Job time: 15 secs

transcription factor 1, POU protein, alternative splice form fruit fly *Drosophila melanogaster*
 CSpecies: *Drosophila melanogaster*
 CDate: 04-Mar-1994 #sequence_revision 1 to 2 1994 #text_change 00-Mar-1994
 CAccession: A42089
 R:Treacy, M.N.; Wells, G.; Li, J.; Turner, R.E.; H-, X.; F. Senfild, Y. T.
 Cell 69, 431-435, 1992
 A>Title: Twin of I-POU, a two amino acid difference in the I-POU home-domain distinguishes
 A:Reference number: A42089; MIM:62154665; PMID:1346754
 A:Accession: A42089
 A>Status: preliminary
 A:Molecule type: PNA
 A:Residues: 1-10 <TRE>
 A:Cross-references: GR:582271; NID:Q245519; PID:Q245518
 A:Note: sequence extracted from NDBI database (NDBI:Q245518) (NDBI:Q245518)
 A:Genetics:
 A:Gene: FlyBase: I-Pou
 A:Cross references: FlyBase: FBgn004419
 Query Match 30.0% Score 27, PP 2, Length 10,
 Best Local Similarity 52.63, Pred. No. 7, 2e+02,
 Matches 4, Conservative 1, Mismatches 3, Indels 0, Gaps 0,
 CY 2 GPKKPKPKS 10
 DB 1 GPKKPKPKS 9
 RESULT 4
 G45681
 off 61.1 phage T6 (fragment)
 CSpecies: phage T6
 CDate: 03-Sep-1993
 CAccession: G45681
 R:Selick, H.B.; Stormo, G.D.; Dyson, R.L.; Alberts, B.M.
 J. Virol. 67, 2305-2316, 1993
 A>Title: Analysis of five presumptive protein coding sequences clustered between the phi
 A:Reference number: A45681; MIM:6418419; PMID:841243
 A:Accession: G45681
 A>Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-16 <PHI>
 A:Note: sequence extracted from NDBI bank (NDBI:G45681)
 Query Match 31.7% Score 27, PP 2, Length 10,
 Best Local Similarity 71.43, Pred. No. 1, 4e+01,
 Matches 5, Conservative 1, Mismatches 4, Indels 0, Gaps 0,
 CY 4 KKKKKYS 10
 DB 4 KKKKKYSN 10
 RESULT 5
 2S albumin large chain (1 and 2) nII - rape (fragments)
 N:Altiturn names: 2S albumin large chain nII
 CSpecies: Brassica napus (rape)
 CDate: 13-Jan-1994 #sequence_revision 1 to 2 1994 #text_change 21-Aug-1994
 CAccession: S04716; S04718; S04717
 R:Monsalvo, P.I.; Moronder, A.; Lopez, L.; Lopez, R.
 FEBS Lett. 353, 200-212, 1990
 A>Title: beta-Turns as structural motifs for the proteolytic processing of seed proteins
 A:Reference number: S04716; MIM:1741174; PMID:1741174
 A:Accession: S04716
 A:Molecule type: PNA
 A:Residues: 1-9, 10, 13 <MON>
 A:Experimental source: seed
 A:Note: 1-9 was also found
 A:Accession: S04718
 A:Molecule type: PNA
 A:Residues: 1-9, 10, 13 <MON>
 A:Experimental source: seed
 A:Accession: S04717

A:Molecule type: protein
 A:Residues: 1-9, 10, 13 <MON>
 A:Experimental source: seed
 Query Match 30.0% Score 26, PP 2, Length 13,
 Best Local Similarity 36.47, Pred. No. 1, 6e+03,
 Matches 4, Conservative 1, Mismatches 4, Indels 0, Gaps 0,
 CY 2 GPKKPKPKS 12
 DB 3 GPKKPKPKS 13
 RESULT 6
 A28719
 thymic humoral factor gamma 2 bovine (fragment)
 CSpecies: Bos primigenius (cattle)
 CDate: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 18-Jun-1991
 CAccession: A28719
 R:Burstein, Y.; Bachner, V.; Pecht, M.; Trainin, N.
 Biochemistry 17, 4069-4071, 1988
 A>Title: Thymic humoral factor gamma 2: purification and amino acid sequence of a protein
 A:Reference number: A28719; MIM:607020; PMID:302194
 A:Accession: A28719
 A:Molecule type: protein
 A:Residues: 1-8 <BUR>
 Query Match 29.3% Score 24, PP 2, Length 8,
 Best Local Similarity 100.0%, Pred. No. 2, 8e+05,
 Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0,
 CY 1 DPKK 4
 DB 3 DPKK 6
 RESULT 7
 S36893
 13.5 kDa protein, myelomonocytic leukaemia (fragment)
 CSpecies: Myelomonocytic leukaemia
 CDate: 13-Jan-1993 #sequence_revision 13-Jan-1993 #text_change 13-Jun-1993
 CAccession: S36893
 R:Chen, N.; Kimura, M.; Higashi, Y.; Yamada, T.
 FEBS Lett. 331, 3-14, 1993
 A>Title: Isolation and amino acid sequence of the 13.5 kDa ribosomal protein in 13.5 kDa
 A:Reference number: S36893; MIM:6404553; PMID:8404553
 A:Accession: S36893
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 <CHA>
 Query Match 29.3% Score 24, PP 2, Length 15,
 Best Local Similarity 66.67, Pred. No. 2, 5e+03,
 Matches 4, Conservative 1, Mismatches 1, Indels 0, Gaps 0,
 CY 1 DPKK 6
 DB 4 DPKK 9
 RESULT 8
 G41383
 13.5 kDa protein, myelomonocytic leukaemia (fragment)
 CSpecies: Myelomonocytic leukaemia
 CDate: 08-May-1993 #sequence_revision 13-May-1993 #text_change 13-Jun-1993
 CAccession: G41383; D41383
 R:Backstadt, T.
 J. Biol. Chem. 268, 7045-7049, 1991
 A>Title: Isolation and amino acid sequence of the 13.5 kDa ribosomal protein in 13.5 kDa
 A:Reference number: G41383; MIM:6404553; PMID:1338008
 A:Accession: G41383
 A>Status: preliminary
 A:Molecule type: protein

QY 5 KKKKKSPK 13
| | | | |
DB 8 KTKKKPPR 16

RESULT 14

PH0137
T-cell receptor: beta chain V-D-J region MS20 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 23 Nov-1991; #Sequence_revision: 23 Nov-1991; #text_change: 20 May-1997
C:Accession: PH0137
R:Martin, R.; Howell, M.D.; Jaraquemada, D.; Flierlage, M.; Richert, J.; Brostoff, S.; Le
C. Exp. Med. 173, 19-24, 1991
A:Title: A myelin basic protein peptide is recognized by cytotoxic T cells in the context
A:Reference number: PH0137; MIM:6106843; PMID:1702137
A:Accession: PH0137
A:Molecule type: mRNA
A:Residues: 1-16 <MAR>
C:Keywords: T-cell receptor

Query Match: 25.6%, Score 21, DB 2, Length 16;
Best Local Similarity: 66.7%, Pred. No. 6.8e+03;
Matches: 4: Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 KKKSPS 12
| | | | |
DB 7 RKDSPS 12

RESULT 15

154379
gene NF2 protein - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 01-Rev 1997; #Sequence_revision: 01 Nov 1997; #text_change: 21 Jul 2000
C:Accession: 154379
R:Arai, E.; Ikeuchi, T.; Nakamura, Y.
Hum. Mol. Genet. 3, 937-939, 1994
A:Title: Characterization of the translocation breakpoint in chromosome 22q12.2 in a fat
A:Reference number: 154379; MIM:6038750; PMID:7951241
A:Accession: 154379
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-9 <RES>
A:Cross-references: GR 972941, NID 5861512, EICH:AA014190.1; PID:G4261890
C:Genetics:
A:Gene: GDB:NF2
A:Cross-references: GDB:120232; OMIM:101000
A:Map position: 22q12.2 q31.2

Query Match: 24.4%, Score 20, DB 2, Length 9;
Best Local Similarity: 57.1%, Pred. No. 2.8e+05;
Matches: 4: Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 KKKKKSP 11
| | | | |
DB 3 RKKKASP 9

Search completed: March 3, 2003, 16:46:37
Job time: 11.6667 secs

Mon Mar :29 2003 us-09-214-913-40.closed.rsp Page 3

Query Match
Best Local Similarity 28.0%; Score 23; DB 1; Length 12;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QV 2 GPKVKKV 9
DB 5 GPKVKKV 12

RESULT 7
CCMW PAT STANDARD; PRI: 13 AA.
ID P80431;
DT 01 NOV 1995 (Pol 32, Created)
DT 01 FEB 1996 (Pol 32, Last sequence update)
DT 16 OCT 2001 (Pol 40, Last annotation update)
DE Cytochrome c oxidase polypeptide with mitochondria; (Fragment).
DE (Fragment).
GN COX7B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Mistar; TISSUE=Liver;
EX MEDLINE=9534529; PubMed=7601165;
FA Schagger H., Neick H., Halangk W., Brandt U., von Jarow M.
RT "Cytochrome c oxidase in developing rat heart: Embryonic priorities and
RT amino-terminal sequences suggest identity of the fetal heart and the
RT adult liver isoform."
RL Eur. J. Biochem. 230:235-241(1995).
CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-ENCODED MITOCHONDRIAL
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL ATPASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -1- CATALYTIC ACTIVITY: 4 ferrocyanide c + O2 -> 4 ferrioxanthione.
CC c + 2 H2O.
KW Oxidoreductase, Mitochondrion.
FT NON TER 10 10
SQ SEQUENCE 10 AA 1210 MW; GPCVGP771A3326 GPC4;
Query Match
Best Local Similarity 24.4%; Score 20; DB 1; Length 10;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0

QV 7 PKVSPS 12
DB 3 OKTIPT 8

RESULT 8
RPOC MYCGA STANDARD; PRI: 13 AA.
ID P47716;
DT 01-FEB-1996 (Pol 33, Created)
DT 01-FEB-1996 (Pol 33, Last sequence update)
DT 16-OCT-2001 (Pol 40, Last annotation update)
DE DNA-directed RNA polymerase beta' chain EC 2.7.7.4. Transcriptase
DE beta' chain) (RNA polymerase beta' subunit) (Fragment).
GN RPOC.
OS Mycoplasma gallisepticum.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmatidae; Mycoplasma.
OX NCBI_TaxID=3096;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A5969Var.B;
FA Stamenov A.V., Poyzvetkaya T.A., Galimov M.A., Poyzvetkaya E.S.,
FA Beabekashvili R.S.;
FA Submitted (XXX-1995) to the EMBL/GenBank/DBJ databases.

```

CC 1 FUNCTION: RNA dependent RNA polymerase catalyzes the transcription
CC OF RNA INTO PNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC 1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC (RNA){N}.
CC 1- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
CC BETA' CHAIN.
CC 1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC
CC This swiss-prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL consortium
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see http://www.isb-sib.ch/announcements
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: L89402; AAC82952.1.
CC Transferrase, RNA directed RNA poly-erase, Transcription.
CC NON_TER 13
CC SEQUENCE 13 AA; 1630 MW; 4BEE22/2/480L4333 CP064;
CC
CC 1- Similarity: 4, Conservative 13, Identical 2, Mismatches 2, Gaps 0.
CC
CC 4 PPTPPT 9
CC 11
CC 6 PPTPPT 13
CC
CC RESULT 9
CC RS19 PPWPBP STANDARD; PRT; 14 AA.
CC
CC DT 30-MAY-2000 (Feb. 19, Created)
CC DT 30-MAY-2000 (Feb. 19, Last sequence update)
CC DT 30-MAY-2000 (Feb. 19, Last annotation update)
CC DE 10s ribosomal protein s19 (Fragment).
CC RPSS NP PPBLA
CC GN pigeon pea witches'-broom phytoplasma.
CC AC Pavia; Pirovano; Molinaro; Acholoplasmataceae;
CC OC Acholoplasmataceae; Phytoplasma
CC OX NCBI_TaxID 37760;
CC RN 11
CC SEQUENCE FROM N.A.
CC MEDLINE=347600; PubMed=347600;
CC PROSITE: P00000; PIRSCAL:16.1; PARTIAL.
CC PW ribosomal protein; rRNA-binding.
CC FT NON TER 1
CC SQ SEQUENCE 14 AA; 1630 MW; 4BEE22/2/480L4333 CP064;
CC
CC 1- FUNCTION: THIS PROTEIN FORMS A COMPLEX WITH S13 THAT BINDS SPECIFICALLY
CC TO THE 16S RIBOSOMAL RNA (RY SIMILARITY).
CC 1- SIMILARITY: BELONGS TO THE S13P FAMILY OF RIBOSOMAL PROTEINS.
CC
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: L27136; AAC82952.1.
CC Transferrase, RNA directed RNA poly-erase, Transcription.
CC NON_TER 13
CC SEQUENCE 13 AA; 1630 MW; 4BEE22/2/480L4333 CP064;
CC
CC 1- Similarity: 4, Conservative 13, Identical 2, Mismatches 2, Gaps 0.
CC
CC 4 PPTPPT 9
CC 11
CC 6 PPTPPT 13
CC
CC RESULT 10
CC RL6 VIBPR STANDARD; PRT; 16 AA.
CC
CC DT 15-DEC-1998 (Feb. 17, Created)
CC DT 15-DEC-1998 (Feb. 17, Last sequence update)
CC DT 15-DEC-1998 (Feb. 17, Last annotation update)
CC DE 4s ribosomal protein L6 (Fragment).
CC RPFL
CC GN Vibrio parvulus (Aeromonas proteolytica).
CC OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrion.
CC OX NCBI_TaxID-671;
CC RN 11
CC SEQUENCE FROM N.A.
CC MEDLINE=37149305; PubMed=8996113;
CC PROSITE: P00000; PIRSCAL:16.1; PARTIAL.
CC PW ribosomal protein; rRNA-binding.
CC FT NON TER 1
CC SQ SEQUENCE 16 AA; 1935 MW; ABC19078DF581B6C CP064;
CC
CC 1- FUNCTION: THIS PROTEIN FORMS A COMPLEX WITH S13 THAT BINDS SPECIFICALLY
CC TO THE 16S RIBOSOMAL RNA (RY SIMILARITY).
CC 1- SIMILARITY: BELONGS TO THE S13P FAMILY OF RIBOSOMAL PROTEINS.
CC
CC This swiss-prot entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U08641; AAC82952.1.
CC Transferrase, RNA directed RNA poly-erase, Transcription.
CC NON_TER 13
CC SEQUENCE 13 AA; 1630 MW; 4BEE22/2/480L4333 CP064;
CC
CC 1- Similarity: 4, Conservative 13, Identical 2, Mismatches 2, Gaps 0.
CC
CC 4 PPTPPT 9
CC 11
CC 6 PPTPPT 13
CC
CC RESULT 11
CC LPCA STAAU STANDARD; PRT; 9 AA.
CC
CC DT 15-DEC-1998 (Feb. 17, Created)
CC DT 15-DEC-1998 (Feb. 17, Last sequence update)
CC DT 15-DEC-1998 (Feb. 17, Last annotation update)
CC DE Chloramphenicol resistance leader peptide.
CC RPFL
CC GN Streptococcus agalactiae.
CC OC Bacteria; Firmicutes; Bacilli; Streptococcaceae; Streptococcus.
CC OX NCBI_TaxID-1089; 1311;
CC RN 11
CC SEQUENCE FROM N.A.
CC MEDLINE=37149305; PubMed=8996113;
CC PROSITE: P00000; PIRSCAL:16.1; PARTIAL.
CC PW ribosomal protein; rRNA-binding.
CC FT NON TER 1
CC SQ SEQUENCE 14 AA; 1630 MW; 4BEE22/2/480L4333 CP064;

```



```

CC or send an email to: llorenzodis@slc.ch
CC
CC EMBL: J03653, AAA44685.1,
CC DR HIV; J03653; TAIISJY1.
CC KW Transcription regulation, Activation, RNA binding, Nuclear protein,
CC MW Aids
CC FT NON TER 1 1
CC SQ SEQUENCE 14 AA; 1453 MW; 37002378F82D7AAB CRC64;
Query March
Best local Similarity 28.63; DB 1; Length 14;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 GPKK 5
DB 11 GPKK 14
RESULT 14
UH09 RAT STANDARD; PRT; 8 AA.
AC P56575;
DT 15-DEC-1998 (rel. 37, Created)
DT 15-DEC-1998 (rel. 37, Last sequence update)
DT 15-DEC-1998 (rel. 37, Last annotation update)
DE Unknown protein from 20-page of heart tissue (Spot P9) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
OC Mammalia; Eutheria, Rodentia, Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
PC STRAIN=Wistar; TISSUE=Heart;
RA Li X, P., Pleissner K. P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RC Submitted (SEP-1998) to the SWISS-PROT data bank.
CC 1 MISTELARFES CM THE ID-DEL THE PTERWINE IT OF THIS UNPHEWN
CC PROTEIN IS: 8.9, ITS MW IS: 42 kDa.
FT NON TER 8
FT SEQUENCE 8 AA; 1029 MW; 95075A6C4140B05 CRC64;
Query March
Best local Similarity 22.0%; Score 19; DB 1; Length 8;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 5 KKKKSP 11
DB 1 QKKRSP 7
RESULT 15
RPP VIPAS STANDARD; PRT; 10 AA.
AC P31351;
DT 01-JUL-1993 (rel. 26, Created)
DT 01-FEB-1994 (rel. 28, Last sequence update)
DT 01-FEB-1994 (rel. 28, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting
DE enzyme inhibitor)
OS Vipera aspis (Aspic viper).
OC Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
OC Reptiles; Squamata; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Vipera.
OX NCBI_TaxID=8706;
RN [1]
RP SEQUENCE.
PC TISSUE=Venom;
RA MFWINE-0042-14; PubMed-2169439;
RA Kowori Y., Sugihara H.;
RT "Characterization of a new inhibitor for angiotensin converting
RT enzyme from the venom of Vipera aspis aspis."
PL Int. J. Biochem. 22:767-771(1990).
CC FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE

```

```

CC ANGIOTENSIN CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC II ACTS AS AN INSUFFICIENT PROTECTIVE AGENT.
CC DR PIR; A60377; XASNEC.
CC KW Hypertensive agent, Venim.
CC FT MOD RES 1 1
CC SQ SEQUENCE 10 AA; 1050 MW; 37A270077F5E77A CRC64;
Query March
Best local Similarity 22.0%; Score 19; DB 1; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GPK 4
DB 5 GPK 7
Search completed: March 3, 2003, 06:42:08
Job time : 6.66667 secs

```


EMBL

L27047

AF483948.1

FT

NON TER

1

SQ

SEQUENCE

14 AA; 1712 MW; 40C478EPAPFFFA4A (CRF4);

Query Match

29.3%; Score 24; DB 2; Length 14;

Best Local Similarity

50.0%; Pred. No. 3, 1e+03;

Matches

6; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY

2 GPKKKKKKSPSK

13

DB

3 GHAKKKKKCKK

14

RESULT 9

Q9R541

ID

Q9R541

AC

Q9R541

DT

01-MAY-2000

(TREMBLrel. 13, Created)

DT

01-MAY-2000

(TREMBLrel. 13, Last sequence update)

DT

01-JUN-2000

(TREMBLrel. 14, Last annotation update)

DE

30S ribosomal protein (Fragment)

CS

Mycobacterium bovis

OC

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae

OC

Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium

OX

NCBI_TaxID=1765;

RN

[1]

RP

SEQUENCE

RX

MEDLINE=94039553; PubMed=9405418;

RA

Chara N., Kimura M., Higashi Y., Yamada T.

RT

"Isolation and amino acid sequence of the 30S ribosomal protein P19

from Mycobacterium bovis BCG";

RL

FEBS Lett. 331:9-14(1993);

SQ

SEQUENCE

15 AA; 1760 MW; 4A345644E019225 (P064);

Query Match

29.3%; Score 24; DB 2; Length 15;

Best Local Similarity

66.7%; Pred. No. 3, 2e+03;

Matches

4; Conservative

1; Mismatches

1; Indels

0; Gaps

0;

CY

1 ESKPK 6

DB

4 EGPRTK 9

RESULT 10

Q9NZH9

ID

Q9NZH9

AC

Q9NZH9

DT

01-OCT-2000

(TREMBLrel. 15, Created)

DT

01-OCT-2000

(TREMBLrel. 15, Last sequence update)

DT

01-OCT-2000

(TREMBLrel. 15, Last annotation update)

DE

Fibroblast growth factor homologous factor 2 isoform 10.1Y

(Fragment)

GN

FHF-2

OS

Homo sapiens (Human)

OC

Eukaryota; Metazoa; Chordata; Vertebrata; Eumetazoa; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo

OC

NCBI_TaxID=9606;

RN

[1]

RP

SEQUENCE FROM N.A.

RX

MEDLINE=20112923; PubMed=10644718;

PA

Munoz-Sanguan I., Smallwood P.W., Nathans J.

RT

"Isoform Diversity among Fibroblast Growth Factor Receptor Kinase Factors

RT

Is Generated by Alternative Promoter Usage and Differential

RT

Splicing";

PL

J. Biol. Chem. 275:2599-2607(2000);

DR

EMBL, AF199613; AA31400.1;

FT

NON TER

16

SQ

SEQUENCE

16 AA; 1763 MW; 705D5A9275BC0623 (CRF4);

Query Match

29.3%; Score 24; DB 4; Length 16;

Best Local Similarity

50.0%; Pred. No. 3, 4e+03;

Matches

5; Conservative

2; Mismatches

3; Indels

0; Gaps

0;



XX Claim 11; Page 70; 75pp; English.

XX The present peptide sequence represents a specifically claimed membrane

XX binding element. The invention relates to a soluble derivative (A) of a

XX soluble polypeptide (B), which comprises at least one heptapeptide

XX membrane-binding elements (MBE) of low membrane affinity covalently

XX associated with the MBE interact, independently and with thermodynamic

XX additivity, with components of collagen or artificial membranes exposed

XX to extracellular fluids (A) are used to treat disorders treatable with

XX (ii) itself, specifically inflammation or any other complement-related

XX disorder (e.g. neurological disease, graft rejection, myocardial

XX infarction, sepsis, rheumatoid arthritis and many others), including

XX application to subcutaneous devices and rheumatoid disease, but also to

XX treat allergy, induce weight loss, to treat ischaemia or asthma and as

XX immunomodulators for treating multiple sclerosis (A) are administered

XX orally, topically, by injection or inhalation at a 0.1-10 (preferably

XX 0.1-1) mg/kg/day

XX Sequence 16 AA;

Query Match 100.0%; Score 82; DB 13; Length 16;

Best local similarity 100.0%; Pos 1 to 16-05;

Mismatches 0; Conservative 0; WGA+T=0; Indels 0; Gaps 0;

QY 1 DGPFFKFKFKSPKSK 16

DB 1 DGPFFKFKFKSPKSK 16

RESULT 2

AAV58858

ID AAY58858 standard; Peptide; 16 AA.

XX AAY58858;

AC AAY58858;

DT 08-MAY-2000 (first entry)

DF Membrane binding element used in anti-angiogenic polypeptide.

XX Anti-angiogenic, angiogenesis inhibition, membrane binding element,

XX cancer, tumor, therapy.

OS Synthetic.

XX W0200004052 A2.

PN 27 JAN 2000.

PP 16-JUL-1997; 96WO-GB00292.

PR 16-JUL-1998; 98GB-0015595.

XX (ADPP-) ADPROTECH PIC.

PA Smith RAG, Bright JP, Steward M, Cox VP;

PI WPI; 2000 162406/16.

XX New soluble derivative of anti-angiogenic polypeptide useful for

XX treatment of primary and secondary tumors, contains a naturally occurring

XX membrane-binding elements for targeting

XX Claim 12, Page 10, 36pp; English.

XX The present sequence is a claimed example of a lysine rich peptide

XX membrane binding element (MBE) that can be utilised in novel

XX soluble derivatives (ii) of anti-angiogenic polypeptides of the

XX invention (i) (iii) comprises at least one heptapeptide MBEs with low

XX membrane affinity that are covalently attached to a soluble

XX anti-angiogenic polypeptide such as a non-enzymic region of a

XX plasminogen, fragments of related proteins containing lysine

XX binding, fragments of collagen or fibrin, neutralising

XX activities against receptors for cell-cell mediators, and

XX antagonists of integrins involved in angiogenesis. The MBEs

XX interact independently with thermodynamic additivity, with

XX components of the vascular endothelium (ii) provide targeted

XX delivery of the anti-angiogenic polypeptide to cell receptors and

XX delivery of active angiogenesis inhibitors to vascular endothelium,

XX and therefore increase the local concentration and reduce the risk

XX of adverse effects of global processes elsewhere in the vasculature.

XX They are used in a claimed method of treatment of primary or

XX secondary tumour.

XX Sequence 16 AA;

Query Match 100.0%; Score 82; DB 21; Length 16;

Best local similarity 100.0%; Pos 1 to 16-05;

Mismatches 0; Conservative 0; WGA+T=0; Indels 0; Gaps 0;

QY 1 DGPFFKFKFKSPKSK 16

DB 1 DGPFFKFKFKSPKSK 16

RESULT 3

ABB81240

ID ABB81240 standard; peptide; 16 AA.

XX ABB81240;

AC ABB81240;

XX 20-AUG-2002 (first entry)

DE Antibacterial membrane binding peptide SEQ ID NO:7.

XX Antibacterial, glycopeptide, peptide, membrane associating element,

XX bacterial infection, antibiotic, polypeptide, glycopeptide inhibition;

XX antibiotic.

XX Synthetic.

XX W02000236512-A1.

XX 10 MAY 2002

XX 02 MAY 2001; 2001W1-GB0467.

XX 03-NOV-2000; 2000GB-0006924.

XX (UYCA) UNIV CAMBRIDGE TECH SERVICES LTD.

XX (ADPP-) ADPROTECH LTD.

XX Cooper MA, Portley JP;

XX WPI; 2002-471404/40

XX Antibacterial compound, useful for the treatment of a bacterial

XX infection by e.g. gram positive or negative bacteria, comprises a

XX conjugate of glycopeptide and peptide membrane-associating element

XX Claim 7; Page 57; 64pp; English.

XX The present invention describes an anti-bacterial compound (ii), comprising

XX a conjugate of glycopeptide and peptide membrane associating element,

XX (iii) comprises the formula V L W X, where V is a glycopeptide moiety that

XX inhibits peptidoglycan biosynthesis in bacteria, L is a linking group

XX and W is a peptide moiety that binds to a cell wall or a membrane-

XX insertive element. Also described (iv) a method of treating or preventing

XX a bacterial infection, comprising the administration of (ii), and (v) use

XX of (ii) in the manufacture of a medicament for the treatment or prevention

XX of a bacterial infection. (ii) are used in the manufacture of a medicament

XX for the treatment or prevention of a bacterial infection in a human or

XX animal body, including both the gram positive and gram negative bacteria

XX including *Staphylococcus* sp., *Enterococcus* sp., *Streptococcus* sp.,

XX *Staphylococcus* sp., *Vibrio* sp., *Helicobacter* sp., *Shigella* sp.,

XX *Escherichia* sp., *Neisseria* sp., *Haemophilus* sp., *Legionella* sp.,

Best Local Similarity 100.0%; Pred. No. 8e-05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 7
AAW45882
ID AAW45882 standard; peptide, 14 AA.
XX
AC AAW45882;
XX
XX 10-JUN-1998 (first entry)
XX Peptide membrane binding element.
XX
XX Membrane binding element, thrombotic disease; inflammation;
KW complement-related disease; soluble peptide.
XX
XX Synthetic.
XX
XX WO9802454-A2.
XX
XX 22-JAN-1998.
XX
XX 08-JUL-1997; 97WO-EP03715.
XX
XX 15-JUN-1996; 96EP-0014871.
XX
XX (ADPR-) ADPROTECH PLC.
XX
XX Gold I, Mossakowska RPI, Smith RAS;
XX
XX WPI; 1998-110524/10.
XX
XX Derivatives of soluble poly-peptides bonded to low affinity
PT membrane binding groups - useful for treating complement related and
PT thrombotic diseases, providing improved localisation at cellular
PT membranes
XX
XX Claim 11; Page 70; 75pp; English.

XX The present peptide sequence represents a specifically claimed membrane
CC binding element. The invention relates to a soluble derivative (A) of a
CC stable polypeptide (P), which exhibits at least one biological
CC membrane binding element (MDE) of low membrane affinity. Namely,
CC associated with (i) WPI, in part, independently and with thermodynamic
CC activity, with components of cellular or artificial membranes exposed
CC to extracellular fluids. (A) are used to treat disorders treatable with
CC (i) itself, specifically inflammation, e.g. any other disorder related
CC directly or indirectly to a biological disease, graft rejection, myocardial
CC infarction, reperfusion, rheumatoid arthritis and many others, including
CC application to inducing desensitisation and immunomodulation, but also to
CC treat allergy, induce weight loss, control metabolism of bacteria and as
CC immunomodulators for treating multiple sclerosis. (A) are administered
CC orally, locally, by injection, intravenously, intramuscularly, preferably
CC 0.1-10 mg/kg/day.

XX Sequence 14 AA;
SQ

Query March 31, 2003, Score 40.0, EE 12, Length 14;
Page 1 of 1 (limit 10); 0000, Pred 8e-16;
Matches 10; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY : DDPKPPPPPPPPKSS 13
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 14

RESULT 8
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 9
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 10
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 11
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 12
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 13
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 14
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 15
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 16
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 17
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 18
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 19
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 20
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 21
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 22
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 23
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 24
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 25
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 26
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 27
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 28
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 29
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 30
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 31
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 32
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 33
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 34
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 35
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 36
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 37
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 38
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 39
AAW45882

QY : DDPKPPPPPPPPKSS 15
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1 DDPKPPPPPPPPKSS 15

RESULT 40
AAW45882

QY : DDPKPPPPPPPPKSS 15
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1 DDPKPPPPPPPPKSS 15

RESULT 41
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 42
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
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RESULT 43
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
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RESULT 44
AAW45882

QY : DDPKPPPPPPPPKSS 15
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RESULT 45
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RESULT 46
AAW45882

QY : DDPKPPPPPPPPKSS 15
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RESULT 47
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RESULT 48
AAW45882

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RESULT 49
AAW45882

QY : DDPKPPPPPPPPKSS 15
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RESULT 50
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 51
AAW45882

QY : DDPKPPPPPPPPKSS 15
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1 DDPKPPPPPPPPKSS 15

RESULT 52
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 53
AAW45882

QY : DDPKPPPPPPPPKSS 15
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RESULT 54
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QY : DDPKPPPPPPPPKSS 15
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RESULT 55
AAW45882

QY : DDPKPPPPPPPPKSS 15
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RESULT 56
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
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RESULT 57
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DB : ||| ||| ||| ||| |||
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RESULT 58
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
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RESULT 59
AAW45882

QY : DDPKPPPPPPPPKSS 15
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RESULT 60
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RESULT 61
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
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RESULT 62
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 63
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 64
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 65
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 66
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
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RESULT 67
AAW45882

QY : DDPKPPPPPPPPKSS 15
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1 DDPKPPPPPPPPKSS 15

RESULT 68
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 69
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
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RESULT 70
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 71
AAW45882

QY : DDPKPPPPPPPPKSS 15
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1 DDPKPPPPPPPPKSS 15

RESULT 72
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 73
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 74
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 75
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 76
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 77
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 78
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 79
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 80
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 81
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 82
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 83
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 84
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 85
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 86
AAW45882

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1 DDPKPPPPPPPPKSS 15

RESULT 87
AAW45882

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DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 88
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 89
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 90
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 91
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 92
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 93
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 94
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 95
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 96
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 97
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 98
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 99
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

RESULT 100
AAW45882

QY : DDPKPPPPPPPPKSS 15
DB : ||| ||| ||| ||| |||
1 DDPKPPPPPPPPKSS 15

XX diagnosis, prevention and treatment of ulcerative colitis
XX Example 3; Page 67; 134pp; English.
XX The invention provides a method for the diagnosis, prevention and
XX treatment of ulcerative colitis (UC) using histone H1-like antigen, a
XX porin antigen or a bacteroides antigen as a target antigen. The method
XX comprises: (1) obtaining a sample from the subject;
XX (2) contacting the sample with a histone H1-like antigen, or bacteroides
XX anti-neutrophil cytoplasmic antibody (pANCA) treatment fragment, to form
XX a complex of the histone H1-like antigen, or the pANCA treatment
XX fragment, and antibody to the histone H1-like antigen; and (3) detecting
XX the presence or absence of the complex; where the presence of the
XX complex indicates that the subject has UC. The pANCA treatment
XX fragment, porin antigen and bacteroides antigen are useful in the
XX diagnosis, prevention and treatment of UC. The method can also be used
XX for identifying agents useful for treating UC. Sequence AAY57345-53
XX represent peptides spanning the human histone H1.1 gene product. These
XX were assayed for NANUC-1 and NANUC-2 binding to identify pANCA reactive
XX peptides.
XX Sequence 15 AA;
XX
XX Query March 48 48; Score 47; DB 20; Length 15;
XX Best Local Similarity 58.3%; Pred. No. 19;
XX Matches 7; Conservative 2; Mismatches 3; Gaps 0;
XX
XX QY 3 PPKKKKKSPKRS 14
XX ||||| |||||
XX DB 3 PPKSAKATPKKZA 14
XX
XX RESULT 14
XX AAY57345
XX ID AAY57345 standard; peptide; 15 AA.
XX AC AAY57345;
XX XX
XX DT 13-JUN-2000 (first entry)
XX XX
XX DE Human histone H1 pANCA-reactive peptide.
XX KW Ulcerative colitis; inflammatory bowel disease; porin antigen;
XX pANCA; perinuclear anti-neutrophil cytoplasmic antibody; human;
XX histone H1; isoform; NANUC-2.
XX XX
XX OS Homo sapiens.
XX XX
XX PN US6033864-A.
XX XX
XX PD 07-MAR-2000.
XX XX
XX PF 12-MAR-1998; 98US-0041899.
XX XX
XX PR 12-APR-1996; 96US-0057846.
XX PR 11-APR-1997; 97US-0837058.
XX XX
XX PA (REGC) UNIV CALIFORNIA.
XX XX
XX PI Cohavy O, Braun C;
XX XX
XX DR WPI; 2000 255695/22.
XX XX
XX PT Diagnosing ulcerative colitis or susceptibility, by detecting complex
XX formation between microbial porin antigen and perinuclear
XX anti-neutrophil cytoplasmic autoantibodies -
XX XX
XX PS Example 3; Column 30; 49pp; English.
XX XX
XX CC The invention provides a method for diagnosing ulcerative colitis in a
XX subject suspected of having inflammatory bowel disease. The method
XX comprises reacting a patient sample with a porin antigen that is

CC immunologically reaction with pMNA (formation: anti-met-raphid
 CC cytoplasmic antibodies) and detecting formation of a Ag-IgMRA complex
 CC as indicative of ulcerative colitis. The method is used to diagnose
 CC ulcerative colitis or susceptibility to it. Sequences AAY57341-351
 CC represent pMNA reactive peptides, derived from human histone H1.
 XX
 SQ Sequence 15 AA;

Query Match 49.51; Score 43; EE 21; Length 15;
 Best local similarity 59.34; Prod No. 19;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 PKKKKKKSPSKS 14
 |||||
 Ch 3 PFFSAFFTFFA 14

RESULT 15

AAR26821
 ID AAR26821 standard; peptide; 9 AA.

XX AC AAR26821;

XX DT 23 JAN 2001 (first entry)

XX DE Peptidic membrane binding element.

XX KW Organ perfusion, transplantation, storage, antiinflammatory;

XX KW immunosuppressive; vasotropic; complement activation inhibitor;

XX KW allograft rejection; ischaemia reperfusion injury.

XX OS Synthetic.

XX PN WC200053007-A1.

XX PD 14-SEP-2000.

XX PF 08-MAR-2000; 2000UO-GR00834.

XX PR 10-MAR-1999; 99GB-0005503.

XX PA (ADPP-) ADPPOTECH LTD.

XX PI Smith RAG, Pratt JR, Sacks SH;

XX DR WPI; 2000-601320/57.

XX PT Preparation for perfusing organ prior to transplantation or storage
 PT comprises soluble derivative of a soluble polypeptide- which comprises
 PT two heterologous membrane binding elements with low membrane affinity
 PT .

PS Example 2; Page 20; 47pp, English.

XX The present invention relates to formulations and preparations for
 CC perfusing an organ prior to transplantation or storage. The preparation
 CC comprises a soluble derivative of a polypeptide, which has two or more
 CC heterologous membrane binding elements. The membrane binding elements are
 CC capable of interacting, independently and with thermodynamic additivity,
 CC with membrane components of the organ exposed to extracellular perfusion
 CC fluids, and a flush storage solution. The preparation exhibits
 CC antiinflammatory, immunosuppressive and vasotropic activity and works as
 CC a complement activation inhibitor and an inhibitor of cytotoxic T
 CC lymphocyte activity. The preparation is used for preparing an organ prior
 CC to transplantation, storage and for prevention, treatment or
 CC amelioration of a disease or disorder associated with inflammation,
 CC inappropriate complement activation or inappropriate activation of
 CC coagulant or thrombotic processes prior to, during or after
 CC transplantation, storage of an organ. The preparation is useful for
 CC treating hyperacute and acute allograft rejection of transplanted organs
 CC such as kidney, heart, liver or lungs, ischaemia-reperfusion injury in
 CC transplanted organs, xenograft rejection and corneal graft rejection. The
 CC present sequence represents a peptidic membrane binding element used in

CC as example of the preparation of the invention.
 XX Sequence 9 AA;

Query Match 47.61; Score 30; EE 21; Length 9;
 Best local similarity 77.81; Prod No. 7 Re105;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 PKKKKKKSP 11
 |||||
 Ch 1 PKKKKKKKSP 9

Search completed: March 3, 2003, 06:44:32
 Job time: 145 secs


```

; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /notes="Xaa = Ile, Met, Thr, Asn, Lys,
; OTHER INFORMATION: Ser or Ala"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 14
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /notes="Xaa = Cys, Arg, Ser or Gly"
US-09-910-396A-53

Query Match 50.0% Score 41 DB 8 Length 14:
Best Local Similarity 72.7% Pred No 5.4,
Matches 8, Conservative 0, Mismatches 3, Indels 0, Gaps 0,

QY 3 PNYNYKPSKSK 13
|||||
Db 2 PNYNYKPSKSK 13

RESULT 2
US-09-805-301-45
; Sequence 45, Application US/090905301
; Patent No. US20020173456A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Louis C.
; Sparrow, James T.
; Hauer, Jochen
; Mims, Martha P.
; TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
; MACROMOLECULE DELIVERY
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 433 West Fifth Street
; Suite 4700
; City: Los Angeles
; State: California
; Country: U S A
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM PC DOS 6.0
; SOFTWARE: Word Perfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/0905,301
; FILING DATE: 13 Mar 2001
; CLASSIFICATION: Unknown
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/584,043
; FILING DATE: Unknown
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 217/189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: "Xaa" stands for any naturally
; occurring amino acid and
; analogues thereof.
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-910-396A-53

Query Match 47.8% Score 39 DB 9 Length 14:
Best Local Similarity 61.5% Pred No 10:
Matches 8, Conservative 0, Mismatches 5, Indels 0, Gaps 0,
; occurring amino acid and
; analogues thereof.
; SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-09-805-301-46

Query Match 47.8% Score 39 DB 9 Length 14:
Best Local Similarity 61.5% Pred No 10:
Matches 8, Conservative 0, Mismatches 5, Indels 0, Gaps 0,
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US-09-945-249-84

Query Match

Best Local Similarity 47.6%; Score 39; DB 9; Length 11;

Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Cy 4 KKKKKKSPSK 13

||||||| 11

Db 2 KKKKKKSPSK 11

RESULT 6

US-09-805-301-47

Sequence 47, Application US/0985530;

Patent No. US20020173456A1

GENERAL INFORMATION:

APPLICANT: Smith, Louis C.

Hauer, Jochen

Mirs, Martha P.

TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR

MACROMOLECULE DELIVERY

NUMBER OF SEQUENCES: 139

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071 2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB

storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 6.0

SOFTWARE: Word Perfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/805,301

FILING DATE: 12-Mar-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/544,343

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/SECRET NUMBER: 417/189

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

OTHER INFORMATION: "Xaa" stands for any naturally

occurring amino acid and

analogues thereof.

SEQUENCE DESCRIPTION: SEQ ID NO: 47:

US-09-805-301-47

Query Match

Best Local Similarity 47.6%; Score 39; DB 9; Length 11;

Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Cy 4 KKKKKKSPSK 16

||||||| 11

Db 1 KKKKKKSPSK 13

US-09-945-249-84

Query Match

Best Local Similarity 80.0%; Pred. No. 11;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy 4 KKKKKKSPSK 13

||||||| 11

Db 2 KKKKKKSPSK 11

RESULT 6

US-09-805-301-47

Sequence 47, Application US/0985530;

Patent No. US20020173456A1

GENERAL INFORMATION:

APPLICANT: Smith, Louis C.

Hauer, Jochen

Mirs, Martha P.

TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR

MACROMOLECULE DELIVERY

NUMBER OF SEQUENCES: 139

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071 2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB

storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 6.0

SOFTWARE: Word Perfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/805,301

FILING DATE: 12-Mar-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/544,343

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/SECRET NUMBER: 417/189

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

OTHER INFORMATION: "Xaa" stands for any naturally

occurring amino acid and

analogues thereof.

SEQUENCE DESCRIPTION: SEQ ID NO: 47:

US-09-805-301-47

Query Match

Best Local Similarity 80.0%; Pred. No. 11;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 4 KKKKKKSPSK 16

||||||| 11

Db 1 KKKKKKSPSK 13

US-09-945-249-84

Query Match

Best Local Similarity 80.0%; Pred. No. 11;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 4 KKKKKKSPSK 16

||||||| 11

Db 1 KKKKKKSPSK 13

RESULT 6

US-09-805-301-47

Sequence 47, Application US/0985530;

Patent No. US20020173456A1

GENERAL INFORMATION:

APPLICANT: Smith, Louis C.

Hauer, Jochen

Mirs, Martha P.

TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR

MACROMOLECULE DELIVERY

NUMBER OF SEQUENCES: 139

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071 2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB

storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 6.0

SOFTWARE: Word Perfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/805,301

FILING DATE: 12-Mar-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/544,343

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/SECRET NUMBER: 417/189

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

OTHER INFORMATION: "Xaa" stands for any naturally

occurring amino acid and

analogues thereof.

SEQUENCE DESCRIPTION: SEQ ID NO: 47:

US-09-805-301-47

Query Match

Best Local Similarity 80.0%; Pred. No. 11;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 4 KKKKKKSPSK 16

||||||| 11

Db 1 KKKKKKSPSK 13

US-09-945-249-84

Query Match

RESULT 7

US-09-806-301-103
 ? Sequence 103, Application US/09/2003/1
 ? Patent No. US20030173456A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Smith, Louis C.
 ? Sparrow, James T.
 ? Hauer, Jochen
 ? Mims, Martha P.
 ? TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
 ? MACROMOLECULE DELIVERY
 ? NUMBER OF SEQUENCES: 103
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Lynn S. Lynn
 ? STREET: 633 West Fifth Street
 ? Suite 4700
 ? CITY: Los Angeles
 ? STATE: California
 ? COUNTRY: U.S.A.
 ? ZIP: 90071-2066
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ? storage
 ? COMPUTER IBM Compatible
 ? OPERATING SYSTEM: MS-DOS 6.0
 ? SOFTWARE: Word Perfect 6.1
 ? CURRENT APPLICATION NUMBER: US/09/2003/1
 ? APPLICATION DATE: 12 Mar 2003
 ? CLASSIFICATION: Unknown
 ? PRI-A APPLICATION DATA:
 ? APPLICATION NUMBER: 08/084,043
 ? FILING DATE: Unknown
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Warburg, Richard J.
 ? REGISTRATION NUMBER: 32,527
 ? REFERENCE/DOC#ET NUMBER: 217/190
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (213) 489-1600
 ? TELEFAX: (213) 955-0440
 ? TELEX: 67-4510
 ? INFORMATION FOR SEQ ID NO: 103:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 15 amino acids
 ? TYPE: amino acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: peptide
 ? SEQUENCE DESCRIPTION: SEQ ID NO: 103:
 US-09-806-301-103

Query Match 47.6%; Score 39; PR 9; Length 15;
 Best Local Similarity 41.5%; Pred. No. 11;
 Matches 9; Conservative 7; Mismatches 5; Indels 0; Gaps 0

QY 4 KKKKKKKKKK 13
 DB 1 KKKKKKKKKK 13

RESULT 8

US-09-214-913-40
 ? Sequence 2, Application US/09/2003/412
 ? Patent No. US20030173456A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Merck & Co., Inc.
 ? Applicant: Dinsmore, Christopher J.
 ? APPLICANT: Bergman, Jeffrey M.
 ? TITLE OF INVENTION: PRENYL-PROTEIN TRANSFERASE INHIBITORS
 ? FILE REFERENCE: 200406
 ? CURRENT APPLICATION NUMBER: US/09/2003/412

CURRENT FILING DATE: 2001-02-16
 PRICE APPLICATION NUMBER: 50/183,451
 PRICE FILING DATE: 2000-02-18
 NUMBER OF SEQ ID NOS: 21
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 15
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: completely synthetic sequence
 US-09-784-818-2

Query Match 47.6%; Score 39; DB 9; Length 15;
 Best Local Similarity 40.0%; Pred. No. 11;
 Matches 9; Conservative 7; Mismatches 1; Indels 0; Gaps 0

QY 4 KKKKKKKKKK 13
 DB 2 KKKKKKKKKK 11

RESULT 9

US-09-770-967-2
 ? Sequence 2, Application US/09/2003/967
 ? Patent No. US200301844A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Verck & Co., Inc.
 ? APPLICANT: Dinsmore, Christopher J.
 ? APPLICANT: Bergman, Jeffrey M.
 ? TITLE OF INVENTION: Inhibitors of Prenyl Protein Transferase
 ? FILE REFERENCE: 200405
 ? CURRENT APPLICATION NUMBER: US/09/2003/967
 ? CURRENT FILING DATE: 2001-02-16
 PRICE APPLICATION NUMBER: 40/143,651
 PRICE FILING DATE: 2000-02-18
 NUMBER OF SEQ ID NOS: 21
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 15
 TYPE: PRT
 ORGANISM: Homo sapien
 US-09-770-967-2

Query Match 47.6%; Score 39; DB 10; Length 15;
 Best Local Similarity 40.0%; Pred. No. 11;
 Matches 9; Conservative 7; Mismatches 1; Indels 0; Gaps 0

QY 4 KKKKKKKKKK 13
 PR 2 KKKKKKKKKK 11

RESULT 10

US-09-806-301-103
 ? Sequence 103, Application US/09/2003/1
 ? Patent No. US20030173456A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Merck & Co., Inc.
 ? Applicant: Williams, Theresa M.
 ? APPLICANT: Stump, Craig A.
 ? TITLE OF INVENTION: Inhibitors of Prenyl Protein Transferase
 ? FILE REFERENCE: 200673
 ? CURRENT APPLICATION NUMBER: US/09/2003/369
 ? CURRENT FILING DATE: 2001-06-16
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 15
 TYPE: PRT
 ORGANISM: Homo sapien

Query Match 47.6% Score 39; DB 10; Length 15;
Best Local Similarity 80.0% Pred. No. 11;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QV 4 KKKKKKSPSK 13
DB 2 KKKKKKSKTK 11

RESULT 13
US-09-784-897A-2
Sequence 2, Application US/8974897A
Patent No. US20020052463A1
GENERAL INFORMATION:
APPLICANT: Merck & Co., Inc.
APPLICANT: Dinsmore, Christopher J.
APPLICANT: Bergman, Jeffrey M.
TITLE OF INVENTION: FENIL PROTEIN TRANSFERASE INHIBITORS
FILE REFERENCE: 20497
CURRENT APPLICATION NUMBER: US/09/784,897A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 65/183,449
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: completely synthetic sequence
US-09-784-897A-2

Query Match 47.6% Score 39; DB 10; Length 15;
Best Local Similarity 80.0% Pred. No. 11;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QV 4 KKKKKKSPSK 13
DB 2 KKKKKKSKTK 11

RESULT 14
US-09-770-983-2
Sequence 2, Application US/09770983
Patent No. US20020052380A1
GENERAL INFORMATION:
APPLICANT: Merck & Co., Inc.
APPLICANT: Dinsmore, Christopher J.
APPLICANT: Bergman, Jeffrey M.
TITLE OF INVENTION: Inhibitors of Protein Protein Transferase
FILE REFERENCE: 20309
CURRENT APPLICATION NUMBER: US/09/770,983
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/193,450
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 15
TYPE: PRT
ORGANISM: Homosapien
US-09-770-983-2

QV 4 KKKKKKSPSK 13
DB 2 KKKKKKSKTK 11

Query Match 47.6% Score 39; DB 10; Length 15;
Best Local Similarity 80.0% Pred. No. 11;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QV 4 KKKKKKSPSK 13
DB 2 KKKKKKSKTK 11

RESULT 13
US-09-784-897A-2
Sequence 2, Application US/8974897A
Patent No. US20020052463A1
GENERAL INFORMATION:
APPLICANT: Merck & Co., Inc.
APPLICANT: Dinsmore, Christopher J.
APPLICANT: Bergman, Jeffrey M.
TITLE OF INVENTION: FENIL PROTEIN TRANSFERASE INHIBITORS
FILE REFERENCE: 20497
CURRENT APPLICATION NUMBER: US/09/784,897A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: 65/183,449
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: completely synthetic sequence
US-09-784-897A-2

Query Match 47.6% Score 39; DB 10; Length 15;
Best Local Similarity 80.0% Pred. No. 11;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QV 4 KKKKKKSPSK 13
DB 2 KKKKKKSKTK 11

RESULT 14
US-09-770-983-2
Sequence 2, Application US/09770983
Patent No. US20020052380A1
GENERAL INFORMATION:
APPLICANT: Merck & Co., Inc.
APPLICANT: Dinsmore, Christopher J.
APPLICANT: Bergman, Jeffrey M.
TITLE OF INVENTION: Inhibitors of Protein Protein Transferase
FILE REFERENCE: 20309
CURRENT APPLICATION NUMBER: US/09/770,983
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/193,450
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 15
TYPE: PRT
ORGANISM: Homosapien
US-09-770-983-2

QV 4 KKKKKKSPSK 13
DB 2 KKKKKKSKTK 11

RESULT 15

US-09-828-325A-3
? Sequence 3, Application US/0929325A
? Patent No. US20020068747A1
? GENERAL INFORMATION:
? APPLICANT: Merck & Co., Inc.
? APPLICANT: Craig A. Stump
? APPLICANT: Theresa M. Williams
? TITLE OF INVENTION: INHIBITORS OF KENYL PROTEIN TRANSFERASE
? FILE REFERENCE: 20636Y
? CURRENT APPLICATION NUMBER: US/09/028,325A
? CURRENT FILING DATE: 2001-08-17
? PRIOR APPLICATION NUMBER: 60/196,244
? PRIOR FILING DATE: 2000-04-10
? NUMBER OF SEQ ID NOS: 25
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 3
? LENGTH: 15
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Completely Synthetic Amino Acid Sequence
US-09-828-325A-3

Query Match 47.6%; Score 39; EE 10; Length 15;
Best Local Similarity 80.0%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKKKKKSPSK 13
||| ||| :
Db 2 KKKKKKSKTK 11

Search completed: March 3, 2003, 06:55:21
Job time : 8 secs


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Db      3 PYKSYKTPKXA 14
RESULT 2
US-08-617-096-15
Sequence 17, Application US/08617064
Patent No. 634436
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Targan, Stephan P.
APPLICANT: Eguchi, Mark
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Bacteremia, Septicemia, Colitis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Heparin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Plater LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,964
FILING DATE: 27 APR 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 69/321,625
FILING DATE: 16-FEB-1993
CLASSIFICATION: 435
REGISTRATION NUMBER: US 67/622,011
FILING DATE: ADAMPTED
CLASSIFICATION: 435
APPLICATION NUMBER: Filing 69/321,625
FILING DATE: 18 APR 1991
CLASSIFICATION: 435
APPLICATION NUMBER: US 67/615,715
FILING DATE: 20 NOV 1990
CLASSIFICATION: 435
APPLICATION NUMBER: US 67/615,706
FILING DATE: 19 APR 1990 (ADAMPTED)
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCET NUMBER: 617-429,964
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 418-3000
TELEFAX: (619) 783-7679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US 08 429-964-77

Query Match          49.8%, Score 40; DB 3; Length 15;
Best Local Similarity 69.3%, Freq. No. 5, C,
Matches              7; Conservative   2; Mismatches    3; Indels     0; Gaps      0;

CY      3 PYKSYKTPKXS 14
Db      3 PYKSYKTPKXA 14
RESULT 3
US-08-429-964-77
Sequence 17, Application US/0842994
Patent No. 5962242
GENERAL INFORMATION:
APPLICANT: BROWN, MICHAEL S.
APPLICANT: GALLAGHER, JOSEPH L.
APPLICANT: BEISS, RYUJI
APPLICANT: CAMPS, GUY E.
TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF PARASITIC
TITLE OF INVENTION: TRANSFERASE INHIBITORS
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD WHITE & DIERKE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 77210

Query Match          47.6%, Score 39; DB 2; Length 17;
Best Local Similarity 80.6%, Freq. No. 4, I,
Matches              9; Conservative  1; Mismatches    1; Indels     1; Gaps      0;

CY      4 PYKPYKSPSK 13
Db      1 KKKPKSKTK 10
RESULT 4
US-08-594-043A-45
Sequence 45, Application US/08584043A
Patent No. 6344436
GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
APPLICANT: Sparrow, James T.
APPLICANT: Haver, Jocheen
APPLICANT: Miwa, Martha P.
TITLE OF INVENTION: LIPOPHTIC PEPTIDES FOR
TITLE OF INVENTION: NATIONWIDE DELIVERY
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90011-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette 1.44 Mb

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Patent
F.A.
Beressa M.
CHIRITERS OF FARNESYL IP
ANSPERASE
4

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F.A.
Beressa M.
CHIRITERS OF FARNESYL IP
ANSPERASE
4

Patent
F.A.
Beressa M.
CHIRITERS OF FARNESYL IP
ANSPERASE
4

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F.A.
Beressa M.
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ANSPERASE
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Beressa M.
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ANSPERASE
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Beressa M.
CHIRITERS OF FARNESYL IP
ANSPERASE
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,712A
FILING DATE:
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,124
FILING DATE: 03-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 19849Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3903
TELEFAX: 908-594-4720
TELEX:

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-984-732A-1

Query Match 47.6%; Score 39; DB 3; Length 15;
Best Local Similarity 80.0%; Pred. No. 7.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKKKKKSPV 13
|||||||
DB 2 KKKKKKSTK 11

RESULT 11

US-09-195-578-13
Sequence 13, Application US/09195578
Patent No. 6054466
GENERAL INFORMATION:
APPLICANT: Ciccione, Terrence M.
APPLICANT: desolms, Jane S. J.
TITLE OF INVENTION: INHIBITORS OF FARNESYL-PROTEIN
TRANSFERASE
FILE REFERENCE: 20121Y
CURRENT APPLICATION NUMBER: US/09/195,578
CURRENT FILING DATE: 1998-11-18
EARLIER APPLICATION NUMBER: 60/067,552
EARLIER FILING DATE: 1997-12-04
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 13
LENGTH: 15
TYPE: PRT
ORGANISM: Homosapien
US-09-195-578-13

Query Match 47.6%; Score 39; DB 3; Length 15;
Best Local Similarity 80.0%; Pred. No. 7.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KKKKKKSPV 13
|||||||
DB 2 KKKKKKSTK 11

RESULT 12

US-09-140-557-13
Sequence 13, Application US/09140557A
Patent No. 6103487
GENERAL INFORMATION:
APPLICANT: Merck & Co., Inc.
APPLICANT: Barnett, Stanley F.
APPLICANT: Heitbrook, David C.

```

; APPLICANT: Haber, Hans E.
; APPLICANT: Faller, Louis E.
; TITLE OF INVENTION: A METHOD OF TREATING CANCER
; FILE REFERENCE: 70-47
; CURRENT APPLICATION NUMBER: US/91/149,557A
; EARLIER FILING DATE: 1998 08 26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthesized peptide substrate for
; OTHER INFORMATION: geranylgeranyl protein transferase type 1
US-09-140-567-13

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Query Match          47.6%; Score 39; DB 3; Length 15;
Best Local Similarity 90.0%; Pred. No. 7.2;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

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```

QY 4 KKKKKKSPSK 13
   |||||
DB 2 KKKKKKSKTK 11

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RESULT 13
US-09-170-951-13
; Sequence 13, Application US/09/170951
; Patent No. 6103721
; GENERAL INFORMATION:
; APPLICANT: Bergman, Jeffrey M.
; APPLICANT: Elmslie, Christopher J.
; APPLICANT: Merck & Co., Inc.
; TITLE OF INVENTION: INHIBITORS OF PAROXYSMAL PROTEIN
; FILE REFERENCE: 1967Y
; CURRENT APPLICATION NUMBER: US/09/170,951
; EARLIER FILING DATE: 1998 10 15
; EARLIER APPLICATION NUMBER: US/09/149,557A
; EARLIER FILING DATE: 1998 10 17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PPT
; ORGANISM: Homosapien
US-09-170-951-13

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Query Match          47.6%; Score 39; DB 3; Length 15;
Best Local Similarity 90.0%; Pred. No. 7.2;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

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QY 4 KKKKKKSPSK 13
   |||||
DB 2 KKKKKKSKTK 11

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RESULT 14
US-09-164-482-13
; Sequence 13, Application US/09/164482A
; Patent No. 6127390
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Desolms, S. Jane
; APPLICANT: Lumma, William C.
; APPLICANT: Shaw, Anthony W.
; APPLICANT: Sisko, John T.
; APPLICANT: Tucker, Thomas J.
; TITLE OF INVENTION: INHIBITORS OF PEROXYL PROTEIN TRANSFERASE

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; FILE REFERENCE: 3963Y
; CURRENT APPLICATION NUMBER: US/09/164,482A
; EARLIER FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: 60/060,871
; EARLIER FILING DATE: 1997 10-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthesized peptide substrate for
; OTHER INFORMATION: geranylgeranyl protein transferase type 1
US-09-164-482-13

```

```

Query Match          47.6%; Score 39; DB 3; Length 15;
Best Local Similarity 90.0%; Pred. No. 7.2;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

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```

QY 4 KKKKKKSPSK 13
   |||||
DB 2 KKKKKKSKTK 11

```

```

RESULT 15
US-09-332-769-2
; Sequence 2, Application US/09/332769
; Patent No. 6172076
; GENERAL INFORMATION:
; APPLICANT: Embrey, Mark W.
; APPLICANT: Perlow, Debra S.
; APPLICANT: Nall, John S.
; APPLICANT: Hoffman, Jacob M.
; TITLE OF INVENTION: INHIBITORS OF PEROXYL PROTEIN
; FILE REFERENCE: 1982Y
; CURRENT APPLICATION NUMBER: US/09/332,769
; EARLIER FILING DATE: 1989-06-14
; EARLIER APPLICATION NUMBER: US 60/089,311
; EARLIER FILING DATE: 1989-06-15
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PPT
; ORGANISM: Homosapien
US-09-332-769-2

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Query Match          47.6%; Score 39; DB 4; Length 15;
Best Local Similarity 90.0%; Pred. No. 7.2;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

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QY 4 KKKKKKSPSK 13
   |||||
DB 2 KKKKKKSKTK 11

```

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Search completed: March 3, 2003, 06:47:02
Job time : 16.6667 secs

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carapace polymerization from Vipera lebetina venom: isolated
MW:156354856; PMID:156354856

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Best Local Similarity 75.0%; Pred. No. 136-04;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query Match 25.7% Score 18; DB 2; Length 12;

Best Local Similarity 75.0%; Pred. No. 136-04;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KDCK 5

Db 5 EDCK 8

RESULT 12

PA0045

Porin p91 - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 30-Jun-1992 #sequence_revision 02 Jan 1993 #text_change 19 Mar-1993

C:Accession: PA0045

P:Kane, M.; Kawakami, T.; Miyatake, N.; Tsuruta, A.

submitted to JIPID, July 1994

A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional

A:Reference number: PA0001

A:Accession: PA0045

A:Molecule type: protein

A:Residues: 1-14 <KAM>

A:Experimental source: root

Query Match 25.7% Score 18; DB 2; Length 14;

Best Local Similarity 75.0%; Pred. No. 136-04;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKCK 7

Db 11 GKCK 14

Query Match 25.7% Score 18; DB 2; Length 12;

Best Local Similarity 75.0%; Pred. No. 136-04;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KDCK 5

Db 5 EDCK 8

RESULT 13

PH1598

13 H Chair V C region (wild type clone 106) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 07-Jun-1994 #sequence_revision 02 Jun 1994 #text_change 10 Mar-1993

C:Accession: PH1598

P:Levinson, R.A.; Garbis-Torres, J.; Leder, P.

J Exp Med 179, 317-329, 1993

A:Title: Molecular characterization of transgene-induced lymphoid leukemia in B cells

A:Reference number: PH1598; MUID:9331609; PMID:9331538

A:Accession: PH1598

A:Molecule type: DNA

A:Residues: 1-14 <LEV>

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match 25.7% Score 18; DB 2; Length 14;

Best Local Similarity 75.0%; Pred. No. 136-04;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKDG 4

Db 2 AKDG 5

Query Match 25.7% Score 18; DB 2; Length 14;

Best Local Similarity 75.0%; Pred. No. 136-04;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKDG 4

Db 2 AKDG 5

RESULT 14

PC0709

unidentified 27.2K protein - mouse (fragment)

Search completed: March 3, 2003, 07:05:09
Job time : 16 secs

Genotools version 1.1.1
1993 - 2003 Genotools Inc.
Using sw model:
14, 07:00:29 : Search time is 10 seconds
(without alignments)
54,070 Million cell updates/sec
18.41
25877 14
by: 0.5
4,476,129 residues
bin: chosen parameters
sub: 4
len: 1000
18: 48 summaries
100%

Result 1
ID RS19_PWWBP STANDARD: PRT: 14 AA.
AC Q52093;
DT 30-MAY-2000 (Ref. 39, Created)
DT 30-MAY-2000 (Ref. 39, Last sequence update)
DT 30-MAY-2000 (Ref. 39, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN RPSS OR RS19.
OS Pigeon pea witches'-broom phytoplasma.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Phytoplasma.
OX NCBI_TaxID=37700;
RN [1]
SF SEQUENCE FROM N.A.
RA MEDLINE-abstract, PubMed-901198;
FA Gundersen E.E., Lee I.M., Rehner S.A., Davis K.E., Kinsbury D.T.,
"Phylogeny of 'Phytoplasma' organisms: phylogenetic analysis of
RT their classification."
BL J. Bacteriol. 176(5244-5254(1994)).
CC -!- FUNCTION: PROTEIN S19 KUNMS A COMPLEX WITH S14 THAT BINDS STRONGLY
CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE S19 FAMILY OF RIBOSOMAL PROTEINS.
CC This SwissProt entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (see <http://www.isb-sib.ch/>
CC or send an email to license@isb-sib.ch).
CC EMBL: L7036; AAA01946.1;
CC InterPro: IPR000202, Ribosomal S19.
CC PROSITE: PS01133, RIBOSOMAL_S19; PARTIAL.
CC Ribosomal protein, rRNA-binding.
CC NCN TER 1 1
CC SEQUENCE 14 AA: 1668 MW: 8514.666 kDa (PDB: 1PBB)
Query Match 41.4%; Score 29; DB 1; Length 14;
Best Local Similarity 60.0%; Pred No. 10-00; 1; Matches 6; Gaps 1;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 1;

47 1 SPCDPEFFK 10
48 |||||
49 5 TDSKPNKK 14
RESULT 2
ID RS19_CLOPP STANDARD: PRT: 14 AA.
AC Q46238;
DT 30-MAY-2000 (Ref. 39, Created)
DT 30-MAY-2000 (Ref. 39, Last sequence update)
DT 30-MAY-2000 (Ref. 39, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN RPSS OR RS19.
OS Pigeon pea witches'-broom phytoplasma.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Phytoplasma.
OX NCBI_TaxID=37700;
RN [1]
SF SEQUENCE FROM N.A.
RA MEDLINE-abstract, PubMed-901198;
FA Gundersen E.E., Lee I.M., Rehner S.A., Davis K.E., Kinsbury D.T.,
"Phylogeny of 'Phytoplasma' organisms: phylogenetic analysis of
RT their classification."
BL J. Bacteriol. 176(5244-5254(1994)).
CC -!- FUNCTION: PROTEIN S19 KUNMS A COMPLEX WITH S14 THAT BINDS STRONGLY
CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE S19 FAMILY OF RIBOSOMAL PROTEINS.
CC This SwissProt entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (see <http://www.isb-sib.ch/>
CC or send an email to license@isb-sib.ch).
CC EMBL: L7036; AAA01946.1;
CC InterPro: IPR000202, Ribosomal S19.
CC PROSITE: PS01133, RIBOSOMAL_S19; PARTIAL.
CC Ribosomal protein, rRNA-binding.
CC NCN TER 1 1
CC SEQUENCE 14 AA: 1668 MW: 8514.666 kDa (PDB: 1PBB)

47 1 SPCDPEFFK 10
48 |||||
49 5 TDSKPNKK 14
RESULT 2
ID RS19_CLOPP STANDARD: PRT: 14 AA.
AC Q46238;
DT 30-MAY-2000 (Ref. 39, Created)
DT 30-MAY-2000 (Ref. 39, Last sequence update)
DT 30-MAY-2000 (Ref. 39, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN RPSS OR RS19.
OS Pigeon pea witches'-broom phytoplasma.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Phytoplasma.
OX NCBI_TaxID=37700;
RN [1]
SF SEQUENCE FROM N.A.
RA MEDLINE-abstract, PubMed-901198;
FA Gundersen E.E., Lee I.M., Rehner S.A., Davis K.E., Kinsbury D.T.,
"Phylogeny of 'Phytoplasma' organisms: phylogenetic analysis of
RT their classification."
BL J. Bacteriol. 176(5244-5254(1994)).
CC -!- FUNCTION: PROTEIN S19 KUNMS A COMPLEX WITH S14 THAT BINDS STRONGLY
CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE S19 FAMILY OF RIBOSOMAL PROTEINS.
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CC entities requires a license agreement (see <http://www.isb-sib.ch/>
CC or send an email to license@isb-sib.ch).
CC EMBL: L7036; AAA01946.1;
CC InterPro: IPR000202, Ribosomal S19.
CC PROSITE: PS01133, RIBOSOMAL_S19; PARTIAL.
CC Ribosomal protein, rRNA-binding.
CC NCN TER 1 1
CC SEQUENCE 14 AA: 1668 MW: 8514.666 kDa (PDB: 1PBB)

J. Bacteriol.

Med 14:5651;
Telius H., Chow L., Ho K., T.P., Ifner T.,human human papillomavirus associated with
tumors of patients with epithelioid dysplasia
(1997).
[11]

WU: 754324032403. 14 AA.

Query Match Score 22; ID 14; Length 8;
Best Local Similarity 42.9%; Pred. No. 5; Mismatches 1; Indels 0; Gaps 0;

J. Bacteriol.

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RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
 RA Hayer W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
 RA Venter J.C.,
 RT "The complete genome sequence of the gastric pathogen *Helicobacter*
 RT pylori".
 RL Nature 389 592-597(1997).
 DR EMBL: AE000559; AAD07512.1;
 DR TIGR: HP0429;
 FW Nucleotide sequence of the *Helicobacter pylori* genome
 SC SEQUENCE 10 AA, 1375 MW, 22050A94E132239 CPGC4;

Query Match 28.6% Score 20, DP 16; Length 12;
 Best Local Similarity 42.9%, Field No. 10-4;
 Matches 3, Conservative 4, Mismatches 0, Indels 0, Gaps 0;

QY 1 SKDGYK 7
 DB 2 NENGKE 8

RESULT 11

Q47693 PRELIMINARY; PRT; 13 AA.
 AC Q47693;
 DT 01-NOV-1996 (TRENDEL 01, Created)
 DT 01-MAY-2000 (TRENDEL 01, Last sequence update)
 DT 01-MAY-2000 (TRENDEL 13, Last annotation update)
 DE Elongation factor T1 (EF T1) (Fragment)
 GN TUFB.
 OS Escherichia coli.
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 83986657; PubMed 7612296.
 RA Hudson L., Rossi J., Landy A.,
 RT "Dual function transcripts specifying tRNA and mRNA".
 RL Nature 324 422-427(1986).
 LR EMBL: X04867; J04777;
 KW Elongation factor, Protein Synthesis.
 FT NON TER 13
 SC SEQUENCE 13 AA, 1017 MW, 0436E8A195E619 D5364;

Query Match 28.6% Score 20, DP 16; Length 12;
 Best Local Similarity 50.0%, Field No. 10-4;
 Matches 4, Conservative 2, Mismatches 0, Indels 0, Gaps 0;

QY 7 YVYGVY 14
 DB 3 KVFPEY 10

RESULT 12

Q9UM69 PRELIMINARY; PRT; 13 AA.
 AC Q9UM69;
 DT 01-MAY-2000 (TRENDEL 13, Created)
 DT 01-MAY-2000 (TRENDEL 13, Last sequence update)
 DT 01-MAY-2000 (TRENDEL 13, Last annotation update)
 DE Elastin (Fragment).
 GN ELN.
 CC Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Eumetazoa; Moll.
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 87374007; PubMed 33384007.
 RA Indik J., Yeh K., Mallow S., Scilla B., Eschenbloom J.,
 PA Pashilam J., Greenstein-Goldstein N.,
 RT "Characterization of the 3' region of the human elastin gene: great at random
 RT of Alu repetitive sequences and few coding sequences".

BL Connect. Tissue Res. 16:197-211(1987).

RP SEQUENCE FROM N.A.
 RX MEDLINE 86000100; PubMed 8970040;
 RA Zhang M.C., He L., Gira M., Yong S.L., Tiller G.E., Davidson J.M.,
 RT "Cutis laxa arising from frameshift mutations in exon 10 of the
 RT elastin gene (ELN)".
 RL J. Biol. Chem 274 941-946(1999).
 DR EMBL: U76476; AA17783.1;
 FW Nucleotide sequence of the human elastin gene
 SC SEQUENCE 13 AA, 1348 MW, 43E1E8E8A8F8D03 F8C64;

Query Match 28.6% Score 20, DP 16; Length 13;
 Best Local Similarity 50.0%, Field No. 10-4;
 Matches 3, Conservative 2, Mismatches 0, Indels 0, Gaps 0;

QY 4 GRKXK 8
 DB 9 GRKXK 13

RESULT 13

Q900X9 PRELIMINARY; PRT; 10 AA.
 AC Q900X9;
 DT 01-MAY-2000 (TRENDEL 13, Created)
 DT 01-MAY-2000 (TRENDEL 13, Last sequence update)
 DT 01-MAY-2000 (TRENDEL 13, Last annotation update)
 DE Large T antigen (Fragment).
 GN Polyomavirus JC.
 CC Viruses; dsDNA viruses; RNA stage; Polyomaviridae; Polyomavirus.
 OC NCBI_TaxID 10932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 86007644; PubMed 10618270;
 RA Bojelli-Mas S., Pina S., Giroues R.,
 RT "Downregulating the expression of polyomaviruses in human
 RT cell populations by studying their presence in urban sewage".
 RL Appl. Environ. Microbiol 66 239-245(2000).
 DR EMBL: AF119345; AA02406.1;
 FW Nucleotide sequence of the polyomavirus JC
 SC SEQUENCE 10 AA, 1093 MW, 47E6A8A8A8A8A8A8 F8C64;

Query Match 27.1% Score 10, DP 12; Length 10;
 Best Local Similarity 50.0%, Field No. 10-4;
 Matches 4, Conservative 0, Mismatches 1, Indels 0, Gaps 0;

QY 9 KSKPT 13
 DB 2 KSKPT 6

RESULT 14

Q900X7 PRELIMINARY; PRT; 10 AA.
 AC Q900X7;
 DT 01-MAY-2000 (TRENDEL 13, Created)
 DT 01-MAY-2000 (TRENDEL 13, Last sequence update)
 DT 01-MAY-2000 (TRENDEL 13, Last annotation update)
 DE Large T antigen (Fragment).
 GN Polyomavirus JC.
 CC Viruses; dsDNA viruses; RNA stage; Polyomaviridae; Polyomavirus.
 OC NCBI_TaxID 10932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 86007644; PubMed 10618270;
 RA Bojelli-Mas S., Pina S., Giroues R.,
 RT "Downregulating the expression of polyomaviruses in human
 RT cell populations by studying their presence in urban sewage".
 RL Appl. Environ. Microbiol 66 239-245(2000).
 DR EMBL: AF119345; AA02406.1;
 FW Nucleotide sequence of the polyomavirus JC

of related proteins containing kringle collagen (K1-1), transforming growth factor- β (TGF- β), and other factors involved in angiogenesis. The MBSs with thermodynamic stability, with clear endothelium, if provided, raised the phenotypic polygenic nature of membranes and vessels, particularly, the fibrotic endothelium, the local concentration and reduce the risk of thrombotic processes elsewhere in the vasculature. New method of treatment of primary or

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 71.4%; Score 50; DR 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

macromolecules, especially for molecule delivery;
the peptide; disease therapy; cell targeting.

identifiers

"any amino acid"

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WHEATINE.

chick Sparrow DT:

macromolecule conjugates used for the

delivery to cells, particularly for gene therapy

English.

A delivery peptide that can be used in the
complex of the invention, the peptide-macromolecule
complex for delivery of a macromolecule into a cell.
The peptide-macromolecule complex comprising a
targetable lipophilic peptide, the complexing a
peptide with a lipid moiety where the delivery
peptide is complexed to the macromolecule. The
peptide-macromolecule complex is used for the
delivery of macromolecules such as nucleic
acids, lipids or carbohydrates. They can be
used for enhancing delivery of genetic material into
cells. They can also be used for assessing human
cells as transgenic animals for assessing human
cells. They can also be used for livestock
cells. The complex is capable of transporting the
peptide and condensed state and releasing the molecule
into the cell. The complex can bind with a cell surface
protein and target the nucleus of the cell.

444 Score 42; ID 14; Length 14;

444 Pred. No. 50;

444 ; Mismatches 4 ; Labels 0; Gaps 0;

444 10 AA.

444

macromolecule protein delivery;
the peptide; disease therapy; cell targeting.

PD 07-MAR-2002.

XX 23 AUG 2001; 2001W0 0006421.

XX 25 AUG 2001; 2001W0 227647P.

PR 07-FEB-2001; 2001GR-0003110.

XX (AVET) AVENTIS PHARM INC.

XX Guo Y, Morse CC, Yao Z, Koosier GA;

XX WPI; 2003-304256/34.

XX New fusion proteins comprising membrane penetrating peptides, useful as

PT in vivo, ex vivo or in vitro intracellular carriers of delivery devices

PT for a compound of interest (e.g. peptide, protein, chemical entity,

PT nucleic acid)

XX Example 2, Page 27, 45pp, English.

XX This invention relates to a novel fusion protein, which comprises a

CC membrane penetrating peptide attached to a compound of interest.

CC The membrane penetrating peptide of the fusion protein is derived from a

CC nuclear localization signal and may be the nuclear localization signal

CC from human period protein hPEP1. The fusion protein is useful for

CC delivery of a compound of interest into a cell. The fusion protein is

CC useful as in vivo, ex vivo or in vitro intracellular delivery devices

CC for a compound of interest (e.g. peptide, protein, chemical entity,

CC nucleic acid). In particular, the polypeptides are useful as protein

CC carriers for delivery of compounds to cells. The present sequence

CC represents the lysine synthetic peptide used in an assay to analyze

CC the ability of different peptides to penetrate cellular membranes in

CC the examples of the invention.

XX Sequence 10 AA;

XX Query Match

XX Post-scan Similarity 98.98; Pred. No. 50;

XX Matches 9; Conservative 0; Mismatches 0; Labels 0; Gaps 0;

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that they can also be used for livestock and the complex is satisfied in supplying the rural population with a minimum of the necessary food. The complex is also equipped with a water surface and a large number of cattle.

Score for
 Fred. No. 7
 Miss
 Score

the macromolecule, uptake, and molecule delivery;
cell peptide; discoloration; cell targeting.

"any amino acid"

NOTES

James C. Wells, Department of Psychiatry

Box 3806

The proposed program of expenditures for the fiscal year 1966 is estimated to be \$1,000,000,000, comprising a total of 1,000,000,000 units of the national currency.

cells. They can also be used to create a transgenic animal by assessing human tel. They can also be used for livestock

and target the nucleus of the cell.

Downloaded from <http://ajphaphysocpharm.sagepub.com/> at 11:06 11 November 2014

Number of hauls	<i>P. setiferus</i> (%)	<i>P. setiferus</i> + <i>P. setiferus</i> + <i>P. setiferus</i> (%)	<i>P. setiferus</i> + <i>P. setiferus</i> + <i>P. setiferus</i> (%)
1	~10	~20	~70
2	~15	~25	~60
3	~20	~30	~50
4	~25	~35	~40
5	~30	~40	~30
6	~35	~45	~20
7	~40	~50	~10
8	~45	~55	~5
9	~50	~60	~2
10	~55	~65	~1

10

1. *...*
 2. *...*
 3. *...*
 4. *...*
 5. *...*
 6. *...*
 7. *...*
 8. *...*
 9. *...*
 10. *...*

Figure 1 displays a sequence of 16 small images arranged in a 4x4 grid, illustrating the stages of a bird's nest construction. The images show the progression from initial egg-laying to the final completed nest.

1. *Chlorophyll a* (Chl *a*)

[illegible]

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AAW38787
 ID AAW38787 standard; peptide; 13 AA.
 AC AAW38787;
 XX
 DT 30-MAR-1998 (first entry)
 XX
 DE Delivery peptide used in peptide macromolecule complex.
 XX
 KW Delivery peptide; peptide-macromolecule complex; macromolecule delivery;
 KW non-exchangeable lipophilic peptide; disease therapy; cell targeting.
 XX
 OS Synthetic.
 XX
 PN W09725070-A2
 XX
 PD 17-JUL-1997.
 XX
 PF 02-JAN-1997, 97WC-0500454.
 XX
 PR 08-JAN-1996; 96US-0584043.
 XX
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX
 PI Hauer J, Mims MP, Smith LC, Sparrow JT;
 XX
 DP WPI; 1997 372622/34.
 XX
 PT New lipophilic peptide-macromolecule complexes - used for the
 PT delivery of macromolecules to cells, particularly for gene therapy
 XX
 PS Claim 6; Page 83; 106pp; English.
 XX
 CC This sequence represents a delivery peptide that can be used in the
 CC peptide-macromolecule complex of the invention. The peptide-macromolecule
 CC complex of the invention is for delivering a macromolecule into a cell,
 CC and comprises a non-exchangeable lipophilic peptide (LP) comprising a
 CC delivery peptide associated with a lipid moiety, where the delivery
 CC peptide portion of the LP is complexed to the macromolecule. The
 CC complexes can be used for the delivery of macromolecules such as nucleic
 CC acids, proteins, oligonucleotides, lipids or carbohydrates. They can be
 CC used to treat diseases by enhancing delivery of specific nucleic acid to
 CC the appropriate targeted cells. They can also be used to create
 CC transformed cells as well as transgenic animals for assessing human
 CC disease in an animal model. They can also be used for livestock
 CC agricultural purposes. The complex is capable of transporting the
 CC macromolecule in a stable and condensed state and releasing the molecule
 CC into the cellular interior. The complex can bind with a cell surface
 CC receptor, lyse an endosome and target the nucleus of the cell.
 XX
 SQ Sequence 13 AA;

Query Match 57.1%; Score 40; DB 18; Length 13;
 Best Local Similarity 60.2%, Fred. No. 11;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2 KKKKKKKKKKKK 14
 | | | | | | | | | |
 DQ 1 KKKKKKKKKKKK 13

Search completed March 3, 2003, 07:02:52
 Job time : 35 secs


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULAR TYPE: peptide
; FEATURE:
; OTHER INFORMATION: "Xaa" stands for any naturally
; occurring amino acid and
; analogues thereof.
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-805-301-45

Query Match: 69.01; Score 42; DB 9; Length 13;
Best Local Similarity: 69.01; Pred. No. 2.6;
Matches: 9; Conservative: 0; Mismatches: 4; Indels: 0; Gaps: 0;

CY 2 FFFFFFFFFXK 14
DB 1 FFFFFFFFFXK 13

RESULT 2
US-09-805-301-46
; Q-4606-46; Application US0904606A1
; Patent No. US66007345A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Louis C.
; Sparrow, James T.
; Hauer, Jochen
; Mims, Martha P.
; TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
; MACROMOLECULE DELIVERY
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071 2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 6.0
; SOFTWARE: Word Perfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,041
; FILING DATE: 12-Mar-2001
; CLASSIFICATION: <UNKNOWN>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/584,043
; FILING DATE: <UNKNOWN>
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/POCKET NUMBER: 217/189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1800
; TELEFAX: (213) 955-0440
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULAR TYPE: peptide
; FEATURE:
; OTHER INFORMATION: "Xaa" stands for any naturally
; occurring amino acid and
; analogues thereof.
; SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-09-805-301-46

Query Match: 57.11; Score 40; DB 9; Length 14;
Best Local Similarity: 57.11; Pred. No. 3.6;
Matches: 8; Conservative: 0; Mismatches: 2; Indels: 0; Gaps: 0;

CY 5 FFFFFFFFFXK 14
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US/09-805301

0915 C.
James T.
Sparrow,
Jochen
Hauer,
Martha P.
Mims,
LIPOPHILIC PEPTIDES FOR
MACROMOLECULE DELIVERY

11/189
ADDRESS: 633 West Fifth Street
Suite 4700
City: Los Angeles
State: California
Country: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 6.0

SOFTWARE: Word Perfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/805,301

FILING DATE: 12 Mar 2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/584,043

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

FFIPFNNY/COFFFT NUMBER: 217/189

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

OTHER INFORMATION: "Xaa" stands for any naturally

occurring amino acid and

analogues thereof.

SEQUENCE DESCRIPTION: SEQ ID NO: 43:

US-09-805-301-44

Query Match 57.1%; Score 40; DB 9; Length 12;

Best Local Similarity 80.0%; Pred. No: 4.3;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

US-09-805-301-7

Sequence 7, Application US/0905301

Patent No. US2002017946A1

GENERAL INFORMATION:

APPLICANT: Smith, Louis C.

Sparrow, James T.

Hauer, Jochen

Mims, Martha P.

TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR

MACROMOLECULE DELIVERY

NUMBER OF SEQUENCES: 139

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

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APPLICANT: Smith, Louis C.
Sparrow, James T.
Hauer, Jochen
Mims, Martha P.

TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
MACROMOLECULE DELIVERY

NUMBER OF SEQUENCES: 139

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

Suite 4700

City: Los Angeles

State: California

Country: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 6.0

SOFTWARE: Word Perfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/805,301

FILING DATE: 12 Mar 2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/584,043

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

FFIPFNNY/COFFFT NUMBER: 217/189

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 44:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

OTHER INFORMATION: "Xaa" stands for any naturally

occurring amino acid and

analogues thereof.

SEQUENCE DESCRIPTION: SEQ ID NO: 44:

US-09-805-301-44

Query Match 57.1%; Score 40; DB 9; Length 12;

Best Local Similarity 80.0%; Pred. No: 4.3;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

US-09-805-301-7

Sequence 7, Application US/0905301

Patent No. US2002017946A1

GENERAL INFORMATION:

APPLICANT: Smith, Louis C.

Sparrow, James T.

Hauer, Jochen

Mims, Martha P.

TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR

MACROMOLECULE DELIVERY

NUMBER OF SEQUENCES: 139

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

```

1 STREET: 633 West Fifth Street
2 CITY: Suite 4700
3 STATE: Los Angeles
4 COUNTRY: U.S.A.
5 ZIP: 90071-2066
6 COMPUTER READABLE FORM:
7 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
8
9 COMPUTER: IBM Compatible
10 OPERATING SYSTEM: IBM PC DOS 6.0
11 SOFTWARE: Word Perfect 6.1
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: US/09/805,301
14 FILING DATE: 12-Mar-2001
15 CLASSIFICATION: <Unknown>
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: 09/854,043
18 FILING DATE: <Unknown>
19 ATTORNEY/AGENT INFORMATION:
20 NAME: Warburg, Richard J.
21 REFERENCE/DOC# NUMBER: 217/189
22 TELECOMMUNICATION INFORMATION:
23 TELEPHONE: (213) 489-1600
24 TELEFAX: (213) 955-0440
25 TELEX: 67-4510
26 INFORMATION FOR SEQ ID NO: 7:
27 SEQUENCE CHARACTERISTICS:
28 LENGTH: 13 amino acids
29 TYPE: amino acid
30 STRANDEDNESS: single
31 TOPOLOGY: linear
32 MOLECULE TYPE: peptide
33 SEQUENCE DESCRIPTION: SEQ ID NO: 7:
34 US-09-805-301-7
35
36 Query Match 57 18; Score 40; Id 9; Length 13;
37 Best Local Similarity 69.23; Pred No 4.6;
38 Matches 9; Conservation 9; Mismatches 4; Indels 0; Gaps 0;
39
40 QY 2 PGGGYYVYVYVYVYVY 14
41 | | | | | | | | | |
42 DB 1 PGGGYYVYVYVYVYVY 13
43
44 RESULT 7
45 US-09-805-301-101
46 Sequence 101, Application US/09/805,301
47 Patent No US20020173456A1
48 GENERAL INFORMATION:
49 APPLICANT: Smith, Louis C.
50 Sparrow, James T.
51 Hauer, Jochen
52 Mims, Martha P.
53 TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
54 MACROMOLECULE DELIVERY
55 NUMBER OF SEQUENCES: 139
56 REFERENCE ADDRESS:
57 ADDRESSEE: Lyon & Lyon
58 STREET: 633 West Fifth Street
59 Suite 4700
60 CITY: Los Angeles
61 STATE: California
62 COUNTRY: U.S.A.
63 ZIP: 90071-2066
64 COMPUTER READABLE FORM:
65 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
66
67 COMPUTER: IBM Compatible
68 OPERATING SYSTEM: IBM PC DOS 6.0
69 SOFTWARE: Word Perfect 6.1
70 CURRENT APPLICATION DATA:
71 APPLICATION NUMBER: US/09/805,301
72 FILING DATE: 12-Mar-2001
73 CLASSIFICATION: <Unknown>
74 PRIOR APPLICATION DATA:
75 APPLICATION NUMBER: 09/854,043
76 FILING DATE: <Unknown>
77 ATTORNEY/AGENT INFORMATION:
78 NAME: Warburg, Richard J.
79 REFERENCE/DOC# NUMBER: 217/189
80 TELECOMMUNICATION INFORMATION:
81 TELEPHONE: (213) 489-1600
82 TELEFAX: (213) 955-0440
83
84 RESULT 8
85 US-09-805-301-8
86 Sequence 8, Application US/09/805,301
87 Patent No US20020173456A1
88 GENERAL INFORMATION:
89 APPLICANT: Smith, Louis C.
90 Sparrow, James T.
91 Hauer, Jochen
92 Mims, Martha P.
93 TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
94 MACROMOLECULE DELIVERY
95 NUMBER OF SEQUENCES: 139
96 REFERENCE ADDRESS:
97 ADDRESSEE: Lyon & Lyon
98 STREET: 633 West Fifth Street
99 Suite 4700
100 CITY: Los Angeles
101 STATE: California
102 COUNTRY: U.S.A.
103 ZIP: 90071-2066
104 COMPUTER READABLE FORM:
105 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
106
107 COMPUTER: IBM Compatible
108 OPERATING SYSTEM: IBM PC DOS 6.0
109 SOFTWARE: Word Perfect 6.1
110 CURRENT APPLICATION DATA:
111 APPLICATION NUMBER: US/09/805,301
112 FILING DATE: 12-Mar-2001
113 CLASSIFICATION: <Unknown>
114 PRIOR APPLICATION DATA:
115 APPLICATION NUMBER: 09/854,043
116 FILING DATE: <Unknown>
117 ATTORNEY/AGENT INFORMATION:
118 NAME: Warburg, Richard J.
119 REFERENCE/DOC# NUMBER: 217/189
120 TELECOMMUNICATION INFORMATION:
121 TELEPHONE: (213) 489-1600
122 TELEFAX: (213) 955-0440

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/
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90045
/ MEDIUM TYPE: 3.5" Diskette, 1.44 MB
/
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: IBM PC DOS 6.0
/ SOFTWARE: Word Perfect 6.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: 98/09/001
/ FILING DATE: 12 Mar 2001
/ CLASSIFICATION: <unknown>
/
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: 98/584,043
/ FILING DATE: <unknown>
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 217/199
/ REFERENCE/LOCKET NUMBER: 217/199
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 489-0440
/ TELEX: 67-3510
/
/ INFORMATION FOR SEQ ID NO: 100:
/
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 100:
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/ US-09-805-301-100
/
/ Query March 30, 2003; Score 10; DP 9; Length 12;
/ Best Local Similarity 80.0%; Pred No. 5.8,
/ Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
/
/ QY 5 KKKKKKSKTK 14
/ DB 1 KKKKKKSKTK 10
/
/ RESULT 12
/ US-09-805-301-100
/ Sequence 53, Application US/09010386A
/ Patent No. US09010386A
/
/ GENERAL INFORMATION:
/ APPLICANT: Ronald, Pamela C.
/ APPLICANT: Wang, Guo-Liang
/ APPLICANT: Song, Wen-Yuang
/ APPLICANT: Hulbert, Scott
/ APPLICANT: Risher, Todd
/
/ TITLE OF INVENTION: Procedures and Materials for Conferencing
/ TITLE OF INVENTION: Disease Resistance in Plants
/ NUMBER OF SEQUENCES: 53
/
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/
/ MEDIUM TYPE: 3.5" Diskette, 1.44 MB
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Police #1.0, Version #1.20
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/010,386A
/ FILING DATE: 13-AUG-1997

```

```

/
/ CLASSIFICATION:
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bastian, Kevin L.
/ REGISTRATION NUMBER: 34,774
/ REFERENCE/LOCKET NUMBER: 023000-0005005005
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/
/ THE INVENTION FILED IN: 11/2001
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/
/ FEATURE:
/ NAME/KEY: Modified site
/ LOCATION: 13
/
/ OTHER INFORMATION: Applicant "OTHER"
/ OTHER INFORMATION: /note "Xaa - Ile, Met, Thr, Asn, Lys,
/ OTHER INFORMATION: Ser or Arg"
/
/ FEATURE:
/ NAME/KEY: Modified site
/ LOCATION: 14
/
/ OTHER INFORMATION: /product= "OTHER"
/ OTHER INFORMATION: /note "Xaa Cys, Arg, Ser or Gly"
/
/ US-09-805-301-100
/
/ Query March 30, 2003; Score 10; DP 9; Length 14;
/ Best Local Similarity 80.0%; Pred No. 6.7;
/ Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
/
/ QY 5 KKKKKKSKTK 14
/ DB 2 KKKKKKSKTK 12
/
/ RESULT 13
/ US-09-805-301-100
/ Sequence 4, Application US/09005301
/ Patent No. US09005301
/
/ GENERAL INFORMATION:
/ APPLICANT: Smith, Louis C.
/ Sparrow, James T.
/ Hauer, Jochean
/ Mims, Martha P.
/
/ TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
/ MACROMOLECULE DELIVERY
/
/ NUMBER OF SEQUENCES: 139
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lynn & Lyon
/ STREET: 633 West Fifth Street
/ Suite 4700
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 MB
/
/ COMPUTER: IBM compatible
/ OPERATING SYSTEM: IBM PC DOS 6.0
/ SOFTWARE: Word Perfect 6.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/005,301
/ FILING DATE: 12 Mar 2001
/ CLASSIFICATION: <unknown>
/
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: 09/584,043
/ FILING DATE: <unknown>
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 217,199

```


TELEFAX: (713) 789 2679
 TELEX: 79-0924
 INFORMATION FOR SEQ ID NO: 77:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-429-964-77

Query Match: 76.0%; Score 49; DB 2; Length 10;
 Best Local Similarity: 100.0%; Pred. NO. 3.09;
 Matches: 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKKKSKTK 14
 DB 1 KKKKKSKTK 10

RESULT 2
 US-09-429-964-77

Sequence 73, Application US/98429964
 Patent No. 5967243
 GENERAL INFORMATION:
 APPLICANT: BROWN, MICHAEL S.
 APPLICANT: COLESTEIN, JESSIE L.
 APPLICANT: PRYOR, GUY L.
 APPLICANT: JAMES, GUY L.
 TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF TRANSPORT
 TITLE OF INVENTION: TRANSPORT INHIBITORS
 NUMBER OF SEQUENCES: 85
 CORRESPONDENCE ADDRESS:
 ADDRESS: APNOLD, WHITE & DURKEE
 STREET: P.O. BOX 4433
 CITY: HOUSTON
 STATE: TEXAS
 COUNTRY: UNITED STATES OF AMERICA
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
 SOFTWARE: Patent In Release #1.0, Version #1.10
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/98/429,964
 FILING DATE: 27-APR-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/021,625
 FILING DATE: 16-FEB-1993
 CLASSIFICATION: 435
 APPLICATION NUMBER: US 07/820,011
 FILING DATE: ABANDONED
 CLASSIFICATION: 435
 APPLICATION NUMBER: PCT/US/91/2060
 FILING DATE: 19-APR-1991
 CLASSIFICATION: 435
 APPLICATION NUMBER: US 07/615,715
 FILING DATE: 20-NOV-1990
 CLASSIFICATION: 435
 APPLICATION NUMBER: US 07/510,706
 FILING DATE: 18-APR-1990 (ABANDONED)
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: PARKER, DAVID L.
 REGISTRATION NUMBER: 30,165
 REFERENCE/DOCKET NUMBER: ITSD 412/PAP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (713) 789-2679
 TELEX: 79-0924
 INFORMATION FOR SEQ ID NO: 73:

SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-429-964-73

Query Match: 76.0%; Score 49; DB 2; Length 14;
 Best Local Similarity: 100.0%; Pred. NO. 3.09;
 Matches: 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKKKSKTK 14
 DB 1 KKKKKSKTK 10

RESULT 3

US-09-584-043A-45
 Sequence 45, Application US/08584043A
 Patent No. 6344436

GENERAL INFORMATION:
 APPLICANT: Smith, Louis C.
 APPLICANT: Sparrow, James T.
 APPLICANT: Hauer, Jochen
 APPLICANT: Mims, Martha P.
 TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
 TITLE OF INVENTION: MATERNAL-FETAL DELIVERY
 NUMBER OF SEQUENCES: 139
 CORRESPONDENCE ADDRESS:
 ADDRESS: LYON & LYON
 STREET: 633 West Fifth Street
 CITY: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM compatible
 OPERATING SYSTEM: IBM P.C. DOS 6.0
 SOFTWARE: Word Perfect 6.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/98/584,043A
 FILING DATE: January 9, 1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Waiburg, Richard J.
 REGISTRATION NUMBER: 30,327
 REFERENCE/DOCKET NUMBER: 21,4189

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 955-0440
 TELEFAX: (213) 955-0440
 TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 45:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

FEATURE:
 OTHER INFORMATION: "Xaa" stands for any naturally
 OTHER INFORMATION: occurring amino acid and
 OTHER INFORMATION: analogues thereof.
 US-09-584 043A 45

Query Match: 60.0%; Score 42; DB 4; Length 13;
 Best Local Similarity: 67.2%; Pred. NO. 3.3;


```

1 ADDRESS: Lyon & Lyon
2 STREET: 633 West Fifth Street
3 STREET: Suite 4700
4 CITY: Los Angeles
5 STATE: California
6 COUNTRY: U.S.A.
7 ZIP: 90071-2066
8 COMPUTER READABLE FORM:
9 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
10 MEDIUM TYPE: Storage
11 OPERATING SYSTEM: IBM P.C. DOS 6.0
12 SOFTWARE: Word Perfect 6.1
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: 217/189
15 FILING DATE: January 8, 1996
16 CLASSIFICATION: 435
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER:
19 FILING DATE:
20 ATTORNEY/AGENT INFORMATION:
21 NAME: Warburg, Richard J.
22 REGISTRATION NUMBER: 32,327
23 REFERENCE/POCKET NUMBER: 217/189
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: (213) 489-1600
26 TELEFAX: (213) 955-0440
27 TELEFAX: 67-9510
28 INFORMATION FOR SEQ. 1: NO. 43
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 11 amino acids
31 TYPE: amino acid
32 STRANDEDNESS: single
33 TOPOLOGY: linear
34 MOLECULE TYPE: peptide
35 FEATURE:
36 OTHER INFORMATION: "Xaa" stands for any naturally
37 OTHER INFORMATION: occurring amino acid and
38 OTHER INFORMATION: analogues thereof.
39 US 08-584-043A-43

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Query Match 57.1%; Score 40; DP 4; Length 11;
Best Local Similarity 92.0%, Freq No. 5.74
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 5 YYYXXYYXKY 14
DB 2 YYYXXYYXKY 11

RESULT 7
US-08-584-043A-44
1 Sequence 44, Application US-08-584-043A
2 Patent No. 6344436
3 GENERAL INFORMATION:
4 APPLICANT: Smith, Louis C.
5 APPLICANT: Sparrow, James T.
6 APPLICANT: Hauser, Jochen
7 APPLICANT: Mims, Martha P.
8 TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
9 TITLE OF INVENTION: MACROMOLECULE DELIVERY
10 NUMBER OF SEQUENCES: 139
11 CORRESPONDENCE ADDRESS:
12 ADDRESSEE: Lyon & Lyon
13 STREET: 633 West Fifth Street
14 STREET: Suite 4700
15 CITY: Los Angeles
16 STATE: California
17 COUNTRY: U.S.A.
18 ZIP: 90071 2066
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

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1 COMPUTER: IBM Compatible
2 OPERATING SYSTEM: IBM P.C. DOS 6.0
3 SOFTWARE: Word Perfect 6.1
4 CURRENT APPLICATION DATA:
5 APPLICATION NUMBER: 217/189
6 FILING DATE: January 8, 1996
7 CLASSIFICATION: 435
8 PRIOR APPLICATION DATA:
9 APPLICATION NUMBER:
10 FILING DATE:
11 ATTORNEY/AGENT INFORMATION:
12 NAME: Warburg, Richard J.
13 REGISTRATION NUMBER: 32,327
14 REFERENCE/POCKET NUMBER: 217/189
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE: (213) 489-1600
17 TELEFAX: (213) 955-0440
18 TELEFAX: 67-9510
19 INFORMATION FOR SEQ. 1: NO. 44:
20 SEQUENCE CHARACTERISTICS:
21 LENGTH: 12 amino acids
22 TYPE: amino acid
23 STRANDEDNESS: single
24 TOPOLOGY: linear
25 MOLECULE TYPE: peptide
26 FEATURE:
27 OTHER INFORMATION: "Xaa" stands for any naturally
28 OTHER INFORMATION: occurring amino acid and
29 OTHER INFORMATION: analogues thereof.
30 US-08-584-043A-44

```

```

Query Match 57.1%; Score 40; DP 4; Length 12;
Best Local Similarity 92.0%, Freq No. 5.74
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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```

QY 5 YYYXXYYXKY 14
DB 2 YYYXXYYXKY 12

RESULT 8
US-08-584-043A-7
1 Sequence 7, Application US-08-584-043A
2 Patent No. 6344436
3 GENERAL INFORMATION:
4 APPLICANT: Smith, Louis C.
5 APPLICANT: Sparrow, James T.
6 APPLICANT: Hauser, Jochen
7 APPLICANT: Mims, Martha P.
8 TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
9 TITLE OF INVENTION: MACROMOLECULE DELIVERY
10 NUMBER OF SEQUENCES: 139
11 CORRESPONDENCE ADDRESS:
12 ADDRESSEE: Lyon & Lyon
13 STREET: 633 West Fifth Street
14 STREET: Suite 4700
15 CITY: Los Angeles
16 STATE: California
17 COUNTRY: U.S.A.
18 ZIP: 90071 2066
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
21 MEDIUM TYPE: Storage
22 OPERATING SYSTEM: IBM P.C. DOS 6.0
23 SOFTWARE: Word Perfect 6.1
24 CURRENT APPLICATION DATA:
25 APPLICATION NUMBER: 217/189
26 FILING DATE: January 8, 1996
27 CLASSIFICATION: 435
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER:
30 FILING DATE:

```

SUBJ: A
 NAME: A
 NATIONAL: A
 BORN: 12/22
 SEX: M
 DATE OF BIRTH: 12/22/1949
 PLACE OF BIRTH: A
 GRADE: 44

7/19/89
42, 127
SER: 11/189
NAME: N
AGE: 22
HT:

MOLECULE TYPE: peptide
 QS-08-584-043A-101
 Query Match 57.1%;
 Best Local Similarity 59.2%;
 Matches 9, Conservative

[illegible]

Sequence 102, Application US/08584043A

Patent No. 6344436
GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
APPLICANT: Sparrow, James T.
APPLICANT: Hauer, Jochen
APPLICANT: Mims, Martha F.
TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
TITLE OF INVENTION: MATERNAL MILK DELIVERY
NUMBER OF SEQUENCES: 139
REFERENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90011-0668
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 6.0
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,043A
FILING DATE: January 8, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 21/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 489-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
US-08-584-043A-102

Query Match 57.1%, Score 40, DB 4, Length 14,
Best Local Similarity 59.0%, Pred. No. 615,
Matches 9, Conservative 0, Mismatches 4, Indels 0, Gaps 0

QY ? KKKKKKKKKKKK 14

DB ? KKKKKKKKKKKK 14

RESULT 12

US-08-097-830E-1
Sequence 1, Application US/5837830E

Patent No. 5052211
GENERAL INFORMATION:
APPLICANT: Fatic, Massimo
TITLE OF INVENTION: Peptides for Neutralizing the
TITLE OF INVENTION: Toxicity of Lipid A
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hedman, Gibson & Costigan
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,830E
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Costigan, James V.
REGISTRATION NUMBER: 25,659
REFERENCE/DOCKET NUMBER: 576-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (412) 302-8998
TELEFAX: (412) 302-8998
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-097-830E-1

Query Match 55.7%, Score 29, DB 1, Length 10;
Best Local Similarity 60.0%, Pred. No. 67;
Matches 8, Conservative 0, Mismatches 2, Indels 0, Gaps 0

QY 5 KKKKKKKKKK 14

DB 1 KKKKKKKKKK 10

RESULT 13

US-08-456-112B-1
Sequence 1, Application US/0844112B
Patent No. 5334430
GENERAL INFORMATION:
APPLICANT: Fatic, Massimo
TITLE OF INVENTION: IDENTIFICATION OF ANTIBIOTICS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hedman, Gibson & Costigan
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: LEADING EDGE 486
OPERATING SYSTEM: DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,112B
FILING DATE: May 31, 1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Costigan, James V.
REGISTRATION NUMBER: 25,659
REFERENCE/DOCKET NUMBER: 576-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (412) 302-8998
TELEFAX: (412) 302-8998
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid


```

1 Sequence 100, Application US/0554404A
2 Patent No. 6344436
3 GENERAL INFORMATION:
4 APPLICANT: Smith, Louis C.
5 APPLICANT: Sparrow, James T.
6 APPLICANT: Haver, Tschan P.
7 APPLICANT: Mims, Martha P.
8 TITLE OF INVENTION: LIPONILIC PEPTIDES FOR
9 TITLE OF INVENTION: MACROMOLECULE DELIVERY
10 NUMBER OF SEQUENCES: 139
11 CORRESPONDENCE ADDRESS:
12 ADDRESSEE: LYCEN & LYON
13 STREET: 633 West Fifth Street
14 STREET: Suite 4700
15 CITY: Los Angeles
16 STATE: California
17 COUNTRY: U.S.A.
18 ZIP: 90071 2066
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
21 MEDIUM TYPE: storage
22 COMPUTER: IBM Compatible
23 OPERATING SYSTEM: IBM P.C. DOS 6.0
24 SOFTWARE: Word Perfect 6.1
25 CURRENT APPLICATION DATA:
26 APPLICATION NUMBER: US/08/584,043A
27 FILING DATE: January 8, 1996
28 CLASSIFICATION: 435
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER:
31 FILING DATE:
32 ATTORNEY/AGENT INFORMATION:
33 NAME: Warburg, Richard J.
34 REGISTRATION NUMBER: 32,327
35 REFERENCE/DOCKET NUMBER: 217/180
36 TELECOMMUNICATION INFORMATION:
37 TELEPHONE: (213) 489-1660
38 TELEFAX: (213) 955-0440
39 TELEX: 67-3510
40 INFORMATION FOR SEQ ID NO: 100:
41 SEQUENCE CHARACTERISTICS:
42 LENGTH: 12 amino acids
43 TYPE: amino acid
44 STRANDEDNESS: single
45 TOPOLOGY: linear
46 MOLECULE TYPE: peptide
47 PS-08-584-043A-100

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Query Match.          55.78; Score 39; EB 4; Length 14;
Best Local Similarity 80.08; Pred. NC 7.8;
Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1
QY 5 XXXXXXXXXX 14
    ||||| |
Db 1 XXXXXXXXXXXX 10

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Search completed: March 3, 2003, 07:05:29
Job time : 14 secs



Creation date: 09-17-2003
Indexing Officer: HNGUYEN28 - HAO NGUYEN
Team: OIPEBackFileIndexing
Dossier: 09214913

Legal Date: 12-18-2002

No.	Doccode	Number of pages
1	NPL	10

Total number of pages: 10

Remarks:

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